International Nonproprietary Names for Pharmaceutical Substances (INN)

RECOMMENDED International Nonproprietary Names: List 80

Notice is hereby given that, in accordance with paragraph 7 of the Procedure for the Selection of Recommended International Nonproprietary Names for Pharmaceutical Substances [*Off. Rec. Wld Health Org.*, 1955, **60**, 3 (Resolution EB15.R7); 1969, **173**, 10 (Resolution EB43.R9); Resolution EB115.R4 (EB115/2005/REC/1)], the following names are selected as Recommended International Nonproprietary Names. The inclusion of a name in the lists of Recommended International Nonproprietary Names does not imply any recommendation of the use of the substance in medicine or pharmacy.
Lists of Proposed (1–117) and Recommended (1–78) International Nonproprietary Names can be found in *Cumulative List No. 17, 2017* (available in CD-ROM only).

Dénominations communes internationales des Substances pharmaceutiques (DCI)

Dénominations communes internationales RECOMMANDÉES: Liste 80

Il est notifié que, conformément aux dispositions du paragraphe 7 de la Procédure à suivre en vue du choix de Dénominations communes internationales recommandées pour les Substances pharmaceutiques [*Actes off. Org. mond. Santé*, 1955, **60**, 3 (résolution EB15.R7); 1969, **173**, 10 (résolution EB43.R9); résolution EB115.R4 (EB115/2005/REC/1)] les dénominations ci-dessous sont choisies par l'Organisation mondiale de la Santé en tant que dénominations communes internationales recommandées. L'inclusion d'une dénomination dans les listes de DCI recommandées n'implique aucune recommandation en vue de l'utilisation de la substance correspondante en médecine ou en pharmacie.
On trouvera d'autres listes de Dénominations communes internationales proposées (1–117) et recommandées (1–78) dans la *Liste récapitulative No. 17, 2017* (disponible sur CD-ROM seulement).

Denominaciones Comunes Internacionales para las Sustancias Farmacéuticas (DCI)

Denominaciones Comunes Internacionales RECOMENDADAS: Lista 80

De conformidad con lo que dispone el párrafo 7 del Procedimiento de Selección de Denominaciones Comunes Internacionales Recomendadas para las Sustancias Farmacéuticas [*Act. Of. Mund. Salud*, 1955, **60**, 3 (Resolución EB15.R7); 1969, **173**, 10 (Resolución EB43.R9); Résolution EB115.R4 (EB115/2005/REC/1) EB115.R4 (EB115/2005/REC/1)], se comunica por el presente anuncio que las denominaciones que a continuación se expresan han sido seleccionadas como Denominaciones Comunes Internacionales Recomendadas. La inclusión de una denominación en las listas de las Denominaciones Comunes Recomendadas no supone recomendación alguna en favor del empleo de la sustancia respectiva en medicina o en farmacia.
Las listas de Denominaciones Comunes Internacionales Propuestas (1–117) y Recomendadas (1–78) se encuentran reunidas en *Cumulative List No. 17, 2017* (disponible sólo en CD-ROM).

Latin, English, French, Spanish: *Recommended INN*	*Chemical name or description; Molecular formula; Graphic formula*
DCI Recommandée	*Nom chimique ou description; Formule brute; Formule développée*
DCI Recomendada	*Nombre químico o descripción; Fórmula molecular; Fórmula desarrollada*

abrezekimabum #

abrezekimab	immunoglobulin Fab G1-kappa, anti-[*Homo sapiens* IL13 (interleukin 13, IL-13)], neutralizing, humanized monoclonal antibody; VH-(CH1-hinge) gamma1 heavy chain (1-223) [humanized VH (*Homo sapiens* IGHV2-26*01 (80.8%) -(IGHD)-IGHJ4*01 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG1*01, G1m17, K120 (217) (CH1 (121-218), hinge 1-5 (218-223)) (121-223)], (223-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]
abrézékimab	immunoglobuline Fab G1-kappa, anti-[*Homo sapiens* IL13 (interleukine 13, IL-13)], neutralisant, anticorps monoclonal humanisé; VH-(CH1-charnière) chaîne lourde gamma1 (1-223) [VH humanisé (*Homo sapiens* IGHV2-26*01 (80.8%) -(IGHD)-IGHJ4*01 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG1*01, G1m17, K120 (217) (CH1 (121-218), charnière 1-5 (218-223)) (121-223)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]
abrezekimab	inmunoglobulina Fab G1-kappa, anti-[*Homo sapiens* IL13 (interleukina 13, IL-13)], neutralizante, anticuerpo monoclonal humanizado; VH-(CH1-bisagra) cadena pesada gamma1 (1-223) [VH humanizado (*Homo sapiens* IGHV2-26*01 (80.8%) -(IGHD)-IGHJ4*01 (100%)) [8.7.14] (1-120) -*Homo sapiens* IGHG1*01, G1m17, K120 (217) (CH1 (121-218), bisagra 1-5 (218-223)) (121-223)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (87.4%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]

Heavy chain / Chaîne lourde / Cadena pesada

```
QVTLKESGPV LVKPTETLTL TCTVSGFSLT NYHVQWIRQP PGKALEWLGV  50
MWSDGDTSFN SVLKSRLTIS RDTSKSQVVL TMTNMDPVDT ATYYCARDGT 100
IAAMDYFDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSC                              223
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCLASEDIS NYLAWYQQKP GKAPKLLIYH  50
TSRLQDGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ GYRFPLTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 147-203
Intra-L (C23-C104) 23'-88' 134'-194'
Inter-H-L (h 5-CL 126) 223-214'
No N-glycosylation sites / pas de site de N-glycosylation / ningún posición de N-glicosilación

adalimumabum beta #	
adalimumab beta	immunoglobulin G1-kappa, anti-[*Homo sapiens* TNF (tumor necrosis factor (TNF) superfamily member 2, TNFSF2, TNF-alpha, TNFA)], human monoclonal antibody; gamma1 heavy chain (1-451) [*Homo sapiens* VH (IGHV3-9*01 (93.9%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), hinge (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-27*01 (95.8%) -IGKJ1*01 (91.7%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (230-230'':233-233'')-bisdisulfide
adalimumab bêta	immunoglobuline G1-kappa, anti-[*Homo sapiens* TNF (facteur de nécrose tumorale membre 2 de la superfamille du TNF, TNFSF2, TNF-alpha, TNFA)], anticorps monoclonal humain; chaîne lourde gamma1 (1-451) [*Homo sapiens* VH (IGHV3-9*01 (93.9%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), charnière (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-27*01 (95.80%) -IGKJ1*01 (91.7%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230'':233-233'')-bisdisulfure
adalimumab beta	inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNF (factor de necrosis tumoral miembro 2 de la superfamilia del TNF, TNFSF2, TNF-afa, TNFA)], anticuerpo monoclonal humano; cadena pesada gamma1 (1-451) [*Homo sapiens* VH (IGHV3-9*01 (93.9%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), bisagra (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-27*01 (95.80%) -IGKJ1*01 (91.7%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (230-230'':233-233'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGRSLRL SCAASGFTFD DYAMHWVRQA PGKGLEWVSA  50
ITWNSGHIDY ADSVEGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCAKVS 100
YLSTASSLDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                   451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQGIR NYLAWYQQKP GKAPKLLIYA  50
ASTLQSGVPS RFSGSGSGTD FTLTISSLQP EDVATYYCQR YNRAPYTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                     214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22''-96'' 148''-204'' 265''-325'' 371''-429''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 224-214' 224''-214'''
Inter-H-H (h 11, h 14) 230-230'' 233-233''
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
301, 301''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
G0F predominant / prédominant / predominante, G2FS2 (0,10 ± 0,04 %), Man4 (0,00 ± 0,01%)

apadamtasum alfa #	
apadamtase alfa	human metalloproteinase with thrombospondin motifs 13 (metalloproteinase ADAMTS13), produced in Chinese hamster ovary (CHO) cells, glycoform alfa
apadamtase alfa	métalloprotéinase avec thrombospondine motif 13 (métalloprotéinase ADAMTS13) humaine, produite par des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa
apadamtasa alfa	metaloproteinasa con trombospondina-motif 13 (metaloproteinasa ADAMTS13) humana, producida por las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
AAGGILHLEL LVAVGPDVFQ AHQEDTERYV LTNLNIGAEL LRDPSLGAQF 50
RVHLVKMVIL TEPEGAPNIT ANLTSSLLSV CGWSQTINPE DDTDPGHADL 100
VLYITRFDLE LPDGNRQVRG VTQLGGACSP TWSCLITEDT GFDLGVTIAH 150
EIGHSFGLEH DGAPGSGCGP SGHVMASDGA APRAGLAWSP CSRRQLLSLL 200
SAGRARCVWD PPRPQPGSAG HPPDAQPGLY YSANEQCRVA FGPKAVACTF 250
AREHLDMCQA LSCHTDPLDQ SSCSRLLVPL LDGTECGVEK WCSKGRCRSL 300
VELTPIAAVH GRWSSWGPRS PCSRSCGGGV VTRRRQCNNP RPAFGGRACV 350
GADLQAEMCN TQACEKTQLE FMSQQCARTD GQPLRSSPGG ASFYHWGAAV 400
PHSQGDALCR HMCRAIGESF IMKRGDSFLD GTRCMPSGPR EDGTLSLCVS 450
GSCRTFGCDG RMDSQQVWDR CQVCGGDNST CSPRKGSFTA GRAREYVTFL 500
TVTPNLTSVY IANHRPLFTH LAVRIGGRYV VAGKMSISPN TTYPSLLEDG 550
RVEYRVALTE DRLPRLEEIR IWGPLQEDAD IQVYRRYGEE YGNLTRPDIT 600
FTYFQPKPRQ AWVWAAVRGP CSVSCGAGLR WVNYSCLDQA RKELVETVQC 650
QGSQQPPAWP EACVLEPCPP YWAVGDFGPC SASCGGGLRE RPVRCVEAQG 700
SLLKTLPPAR CRAGAQQPAV ALETCNPQPC PARWEVSEPS SCTSAGGAGL 750
ALENETCVPG ADGLEAPVTE GPGSVDEKLP APEPCVGMSC PPGWGHLDAT 800
SAGEKAPSPW GSIRTGAQAA HVWTPAAGSC SVSCGRGLME LRFLCMDSAL 850
RVPVQEELCG LASKPGSRRE VCQAVPCPAR WQYKLAACSV SCGRGVVRRI 900
LYCARAHGED DGEEILLDTQ CQGLPRPEPQ EACSLEPCPP RWKVMSLGPC 950
SASCGLGTAR RSVACVQLDQ GQDVEVDEAA CAALVRPEAS VPCLIADCTY 1000
RWHVGTWMEC SVSCGDGIQR RRDTCLGPQA QAPVPADFCQ HLPKPVTVRG 1050
CWAGPCVGQG TPSLVPHEEA AAPGRTTATP AGASLEWSQA RGLLFSPAPQ 1100
PRRLLPGPQE NSVQSSACGR QHLEPTGTID MRGPGQADCA VAIGRPLGEV 1150
VTLRVLESSL NCSAGDMLLL WGRLTWRKMC RKLLDMTFSS KTNTLVVRQR 1200
CGRPGGGVLL RYGSQLAPET FYRECDMQLF GPWGEIVSPS LSPATSNAGG 1250
CRLFINVAPH ARIAIHALAT NMGAGTEGAN ASYILIRDTH SLRTTAFHGQ 1300
QVLYWESESS QAEMEFSEGF LKAQASLRGQ YWTLQSWVPE MQDPQSWKGK 1350
EGT                                                  1353
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
81-134 128-207 168-191 237-263 248-273 258-292
286-297 322-359 326-364 337-349 376-413 409-448
434-453 458-474 471-481

Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)
Asn-68 Asn-72 Asn-478 Asn-505 Asn-540 Asn-593
Asn-633 Asn-754 Asn-1161 Asn-1280

Glycosylation sites (O) / Sites de glycosylation (O) / Posiciones de glicosilación (O)
Ser-325 Ser-624 Ser-683 Ser-833 Ser-891 Ser-953 Ser-1013

apraglutidum

apraglutide

5,7-O-didephosphono[Ala^{2}>Gly,Met^{10}>Ahx,Asn^{11}>D-Phe,Asn^{16}>Leu]human glucagon-like peptide 2 (1-33)-peptide 33-amide:
L-histidylglycyl-L-α-aspartylglycyl-L-seryl-L-phenylalanyl-L-seryl-L-α-aspartyl-L-α-glutamyl-L-2-aminohexanoyl-D-phenylalanyl-L-threonyl-L-isoleucyl-L-leucyl-L-α-aspartyl-L-leucyl-L-leucyl-L-alanyl-L-alanyl-L-arginyl-L-α-aspartyl-L-phenylalanyl-L-isoleucyl-L-asparaginyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-glutaminyl-L-threonyl-L-lysyl-L-isoleucyl-L-threonyl-L-α-asparagine

apraglutide

5,7-O-didephosphono[Ala^{2}>Gly,Met^{10}>Ahx,Asn^{11}>D-Phe,Asn^{16}>Leu]peptide semblable au glucagon 2 humain (1-33)-peptide 33-amide:
L-histidylglycyl-L-α-aspartylglycyl-L-séryl-L-phénylalanyl-L-séryl-L-α-aspartyl-L-α-glutamyl-L-2-aminohexanoyl-D-phénylalanyl-L-thréonyl-L-isoleucyl-L-leucyl-L-α-aspartyl-L-leucyl-L-leucyl-L-alanyl-L-alanyl-L-arginyl-L-α-aspartyl-L-phénylalanyl-L-isoleucyl-L-asparaginyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-glutaminyl-L-thréonyl-L-lysyl-L-isoleucyl-L-thréonyl-L-α-asparagine

apraglutida

5,7-O-didefosfono[Ala^{2}>Gly,Met^{10}>Ahx,Asn^{11}>D-Phe,Asn^{16}>Leu] péptido similar al glucagón humano 2-(1-33)-péptido 33-amida:
L-histidilglicil-L-α-aspartilglicil-L-seril-L-fenilalanil-L-seril-L-α-aspartil-L-α-glutamil-L-2-aminohexanoil-D-fenilalanil-L-treonil-L-isoleucil-L-leucil-L-α-aspartil-L-leucil-L-leucil-L-alanil-L-alanil-L-arginil-L-α-aspartil-L-fenilalanil-L-isoleucil-L-asparaginil-L-triptofil-L-leucil-L-isoleucil-L-glutaminil-L-treonil-L-lisil-L-isoleucil-L-threonil-L-α-asparagina

$C_{172}H_{263}N_{43}O_{52}$

H-His-Gly-Asp-Gly-Ser-Phe-Ser-Asp-Glu-Ahx-D-Phe-Thr-Ile-Leu-Asp-Leu-Leu-Ala-Arg-Ala-Asp-Phe-Ile-Asn-Trp-Leu-Ile-Gln-Thr-Lys-Ile-Thr-Asp-NH_2

arazasetronum

arazasetron

N-[(3R)-1-azabicyclo[2.2.2]octan-3-yl]-6-chloro-4-methyl-3-oxo-3,4-dihydro-2H-1,4-benzoxazine-8-carboxamide

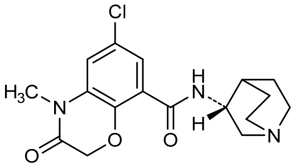
arazasétron

N-[(3R)-1-azabicyclo[2.2.2]octan-3-yl]-6-chloro-4-méthyl-3-oxo-3,4-dihydro-2H-1,4-benzoxazine-8-carboxamide

arazasetrón

N-[(3R)-1-azabiciclo[2.2.2]octan-3-il]-6-cloro-4-metil-3-oxo-3,4-dihidro-2H-1,4-benzoxazina-8-carboxamida

$C_{17}H_{20}ClN_3O_3$



belantamabum #

belantamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)], humanized monoclonal antibody;

	gamma1 heavy chain (1-451) [humanized VH (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01 (85.7%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), hinge (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (230-230":233-233")-bisdisulfide
bélantamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteur du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-451) [VH humanisé (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01(85.7%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), charnière (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230":233-233")-bisdisulfure
belantamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, miembro 17 de la superfamilia del receptor del factor de necrosis tumoral, antígeno de maduración de célula B, BCMA, BCM, TNFRSF13A, CD269)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-451) [VH humanizado (*Homo sapiens* IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01(85.7%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), bisagra (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS NYWMHWVRQA PGQGLEWMGA  50
TYRGHSDTYY NQKFKGRVTI TADKSTSTAY MELSSLRSED TAVYYCARGA 100
IYDGYDVLDN WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                     451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKLLIYY  50
TSNLHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YRKLPWTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                       214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

```
Intra-H (C23-C104)  22-96     148-204     265-325     371-429
                    22"-96"   148"-204"   265"-325"   371"-429"
Intra-L (C23-C104)  23'-88'    134'-194'
                    23'"-88'"  134'"-194'"
Inter-H-L (h 5-CL 126)  224-214'  224"-214'"
Inter-H-H (h 11, h 14)  230-230"  233-233"
```

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
301, 301"
100% afucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes 100% afucosylés / glicanos de tipo CHO biantenarios complejos 100% afucosilados.
G0 > 75%.

C-terminal lysine clipping: H CHS K2: 451, 451" (clipping >90%).

belantamabum mafodotinum #

belantamab mafodotin	immunoglobulin G1-kappa, anti-[_Homo sapiens_ TNFRSF17 (TNF receptor superfamily member 17, tumor necrosis factor receptor superfamily, member 17, B cell maturation antigen, BCMA, BCM, TNFRSF13A, CD269)], humanized monoclonal antibody conjugated to auristatin F; gamma1 heavy chain (1-451) [humanized VH (_Homo sapiens_ IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01 (85.7%)) [8.8.14] (1-121) -_Homo sapiens_ IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), hinge (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (_Homo sapiens_ IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -_Homo sapiens_ IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimer (230-230":233-233")-bisdisulfide; conjugated, on an average of 4 cysteinyl, to monomethylauristatin F (MMAF), via a noncleavable maleimidocaproyl (mc) linker For the _mafodotin_ part, please refer to the document _"INN for pharmaceutical substances: Names for radicals, groups and others"*._
bélantamab mafodotine	immunoglobuline G1-kappa, anti-[_Homo sapiens_ TNFRSF17 (membre 17 de la superfamille des récepteurs du TNF, membre 17 de la superfamille des récepteur du facteur de nécrose tumorale, antigène de maturation de cellule B, BCMA, BCM, TNFRSF13A, CD269)], anticorps monoclonal humanisé conjugué à l'auristatine F; chaîne lourde gamma1 (1-451) [VH humanisé (_Homo sapiens_ IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01(85.7%)) [8.8.14] (1-121) -_Homo sapiens_ IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), charnière (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (_Homo sapiens_ IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -_Homo sapiens_ IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (230-230":233-233")-bisdisulfure; conjugué, sur 4 cystéinyl en moyenne, au monométhylauristatine F (MMAF), via un linker maléimidocaproyl (mc) non clivable Pour la partie _mafodotine_, veuillez-vous référer au document _"INN for pharmaceutical substances: Names for radicals, groups and others"*._
belantamab mafodotina	inmunoglobulina G1-kappa, anti-[_Homo sapiens_ TNFRSF17 (miembro 17 de la superfamilia de los receptores del TNF, miembro 17 de la superfamilia de los receptores del factor de necrosis tumoral, antígeno de maduración de célula B, BCMA, BCM, TNFRSF13A, CD269)], anticuerpo monoclonal humanizado conjugado con la auristatina F; cadena pesada gamma1 (1-451) [VH humanizado (_Homo sapiens_ IGHV1-69*06 (83.7%) -(IGHD)-IGHJ4*01(85.7%)) [8.8.14] (1-121) -_Homo sapiens_ IGHG1*01, G1m17,1 (CH1 K120 (218) (122-219), bisagra (220-234), CH2 (235-344), CH3 D12 (360), L14 (362) (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA humanizado (_Homo sapiens_ IGKV1-33*01 (90.5%) -IGKJ2*02 (100%)) [6.3.9] (1'-107') -_Homo sapiens_ IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (230-230":233-233")-bisdisulfuro; conjugado, en 4 cisteinil por término medio, con monometilauristatina F (MMAF), mediante un enlace maleimidocaproil (mc) no escindible Para la fracción _mafodotina_, se pueden dirigir al documento "_INN for pharmaceutical substances: Names for radicals, groups and others_"*.

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS NYWMHWVRQA PGQGLEWMGA  50
TYRGHSDTYY NQKFKGRVTI TADKSTSTAY MELSSLRSED TAVYYCARGA 100
IYDGYDVLDN WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                      451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKLLIYY  50
TSNLHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YRKLPWTFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 148-204 265-325 371-429
22"-96" 148"-204" 265"-325" 371"-429"
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126)* 224-214' 224"-214'''
Inter-H-H (h 11, h 14)* 230-230" 233-233"
*Two or three of the inter-chain disulfide bridges are not present, an average of 4 cysteinyl being conjugated each via a thioether bond to a drug linker. *Deux ou trois des ponts disulfures inter-chaînes ne sont pas présents, 4 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif. *Faltan dos o tres puentes disulfuro inter-catenarios, una media de 4 cisteinil está conjugada a conectores de principio activo.

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
301, 301"
100% afucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes 100% afucosylés / glicanos de tipo CHO biantenarios complejos 100% afucosilados.
G0 > 75%.

C-terminal lysine clipping:
H CHS K2: 451, 451" (clipping >90%)

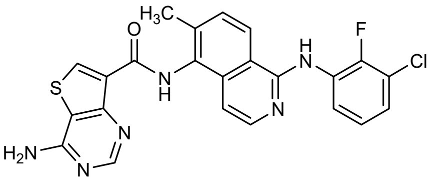
belvarafenibum

belvarafenib 4-amino-*N*-[1-(3-chloro-2-fluoroanilino)-6-methylisoquinolin-5-yl]thieno[3,2-*d*]pyrimidine-7-carboxamide

belvarafénib 4-amino-*N*-[1-(3-chloro-2-fluoroanilino)-6-méthylisoquinolin-5-yl]thiéno[3,2-*d*]pyrimidine-7-carboxamide

belvarafenib 4-amino-*N*-[1-(3-cloro-2-fluoroanilino)-6-metilisoquinolin-5-il]tieno[3,2-*d*]pirimidina-7-carboxamida

$C_{23}H_{16}ClFN_6OS$



bersanlimabum #

bersanlimab immunoglobulin G1-lambda, anti-[*Homo sapiens* ICAM1 (intercellular adhesion molecule 1, ICAM-1, CD54)], human monoclonal antibody;

	gamma1 heavy chain (1-447) [*Homo sapiens* VH (IGHV3-33*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (214) (118-215), hinge (216-230), CH2 (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-216')-disulfide with lambda light chain (1'-217') [*Homo sapiens* V-LAMBDA (IGKV1-40*01 (92.9%) -IGLJ3*02, 91.7%, V2>L (101)) [9.3.11] (1'-111') -*Homo sapiens* IGLC3*04 (112'-217')]; dimer (226-226'':229-229'')-bisdisulfide
bersanlimab	immunoglobuline G1-lambda, anti-[*Homo sapiens* ICAM1 (molécule 1 d'adhésion cellulaire, ICAM-1, CD54)], anticorps monoclonal humain; chaîne lourde gamma1 (1-447) [*Homo sapiens* VH (IGHV3-33*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (214) (118-215), charnière (216-230), CH2 (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-216')-disulfure avec la chaîne légère lambda (1'-217') [*Homo sapiens* V-LAMBDA (IGKV1-40*01 (92.9%) -IGLJ3*02, 91.7%, V2>L (101)) [9.3.11] (1'-111') -*Homo sapiens* IGLC3*04 (112'-217')]; dimère (226-226'':229-229'')-bisdisulfure
bersanlimab	inmunoglobulina G1-lambda, anti-[*Homo sapiens* ICAM1 (molécula 1 de adhesión celular, ICAM-1, CD54)], anticuerpo monoclonal humano; cadena pesada gamma1 (1-447) [*Homo sapiens* VH (IGHV3-33*01 (90.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (214) (118-215), bisagra (216-230), CH2 (231-340), CH3 D12 (356), L14 (358) (341-445), CHS (446-447)) (118-447)], (220-216')-disulfuro con la cadena ligera lambda (1'-217') [*Homo sapiens* V-LAMBDA (IGKV1-40*01 (92.9%) -IGLJ3*02, 91.7%, V2>L (101)) [9.3.11] (1'-111') -*Homo sapiens* IGLC3*04 (112'-217')]; dímero (226-226'':229-229'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS NAWMSWVRQA PGKGLEWVAF  50
IWYDGSNKYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARYS 100
GWYFDYWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
QSVLTQPPSA SGTPGQRVTI SCTGSSSNIG AGYDVHWYQQ LPGTAPKLLI  50
YDNNNRPSGV PDRFSGSKSG TSASLAISGL RSEDEADYYC QSYDSSLSAW 100
LFGGGTKLTV LGQPKAAPSV TLFPPSSEEL QANKATLVCL ISDFYPGAVT 150
VAWKADSSPV KAGVETTTPS KQSNNKYAAS SYLSLTPEQW KSHRSYSCQV 200
THEGSTVEKT VAPTECS                                     217
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	144-200	261-321	367-425
	22''-96''	144''-200''	261''-321''	367''-425''
Intra-L (C23-C104)	22'-90'	139'-198'		
	22'''-90'''	139'''-198'''		
Inter-H-L (h 5-CL 126)	220-216'	220''-216'''		
Inter-H-H (h 11, h 14)	226-226''	229-229''		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
297, 297''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
G0F, G1F

bifikafuspum alfa #

bifikafusp alfa

immunoglobulin single-chain variable fragment anti-(human fibronectin ED-B domain) (1-236), with a GDGSSGGSGGAS linker (117-128) between the VH and VL regions, fused, via a EF(S$_4$G)$_3$ linker (237-253), to human interleukin-2 (IL2) (254-386), non-covalent dimer, produced in mouse hybridoma cells, glycoform alfa:
scFv-IL2 chain (1-386) [*Homo sapiens* VH (IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.9] (1-116) -12-mer linker (117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.8%) -IGKJ1*01 (100%)) [7.3.9] (129-236) -17-mer EF(SSSSG)3 linker (237-253) -*Homo sapiens* IL2 (Pr21-153) (254-386)]; noncovalent dimer

bifikafusp alfa

immunoglobuline à chaîne unique Fragment variable (scFv), anti-(domaine ED-B de la fibronectine humaine) (1-236), avec un linker GDGSSGGSGGAS (117-128) entre les régions VH et VL, fusionnée, via un linker EF(S$_4$G)$_3$ (237-253), à l'interleukine 2 (IL2) humaine (254-386), dimère non covalent, produit par des cellules hybridomes de souris, glycoforme alfa:
chaîne scFv-IL2 (1-386) [*Homo sapiens* VH (IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.9] (1-116) -12-mer linker(117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.80%) -IGKJ1*01 (100%)) [7.3.9] (129-236) -17-mer EF(SSSSG)3 linker (237-253) -*Homo sapiens* IL2 (Pr21-153) (254-386)]; dimère non-covalent

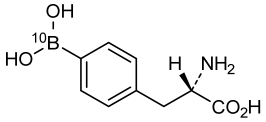
bifikafusp alfa

inmunoglobulina con una cadena única Fragmento variable (scFv), anti-(dominio ED-B de la fibronectina humana) (1-236), con un enlace GDGSSGGSGGAS (117-128) entre las regiones VH y VL, fusionada, a través de un enlace EF(S$_4$G)$_3$ (237-253), con la interleukina 2 (IL2) humana (254-386), dímero no covalente, producido por las células hibridomas de ratón, glicoforma alfa:
cadena scFv-IL2 (1-386) [*Homo sapiens* VH (IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.9] (1-116) -12-mer ligante (117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.80%) -IGKJ1*01 (100%)) [7.3.9] (129-236) -17-mer EF(SSSSG)3 ligante (237-253) -*Homo sapiens* IL2 (Pr21-153) (254-386)]; dímero no covalente

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SFSMSWVRQA PGKGLEWVSS 50
ISGSSGTTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPF 100
PYFDYWGQGT LVTVSSGDGS SGGSGGASEI VLTQSPGTLS LSPGERATLS 150
CRASQSVSSS FLAWYQQKPG QAPRLLIYYA SSRATGIPDR FSGSGSGTDF 200
TLTISRLEPE DFAVYYCQQT GRIPPTFGQG TKVEIKEFSS SSGSSSSGSS 250
SSGAPTSSST KKTQLQLEHL LLDLQMILNG INNYKNPKLT RMLTFKFYMP 300
KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS NINVIVLELK 350
GSETTFMCEY ADETATIVEF LNRWITFCQS IISTLT                386
```

Disulfide bridges location / Positions des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H : 22-96
Intra-L : 151-217
IL2 portion : 311-358

Glycosylation site (O) / Site de glycosylation (O) / Posición de glicosilación (O)
Thr-256

bizalimogenum ralaplasmidum #	
bizalimogene ralaplasmid	a DNA plasmid encoding genes for human papilloma virus type 18 (HPV-18) E6 and E7 proteins whose expression is driven by the human cytomegalovirus (hCMV) promoter with the bovine growth hormone (bGH) 3'end gene and bGH gene polyA signal
bizalimogène ralaplasmide	ADN plasmidique contenant les gènes codant pour les protéines E6 et E7 du virus du papillome humain de type 18 (HPV-18), dont l'expression est dirigée par le promoteur du cytomégalovirus humain (hCMV) avec la région 3'-terminale du gène de l'hormone de croissance bovine (bGH) et le signal poly-A du gène de la bGH
bizalimogén ralaplásmido	un DNA plasmídico que contiene genes que codifican para las proteínas E6 y E7 del virus del papiloma humano tipo 18 (HPV-18), cuya expresión está dirigida por el promotor del citomegalovirus humano (hCMV) con la región 3' terminal del gen de la hormona de crecimiento bovina (bGH) y la señal poli A del gen de bGH
borofalanum (^{10}B)	
borofalan (^{10}B)	4-[(^{10}B)borono]-L-phenylalanine
borofalan (^{10}B)	4-[(^{10}B)borono]-L-phénylalanine
borofalán (^{10}B)	4-[(^{10}B)borono]-L-fenilalanina
	$C_9H_{12}{}^{10}BNO_4$
	
bulevirtidum	
bulevirtide	*N*-tetradecanoylglycyl-L-threonyl-L-asparaginyl-L-leucyl-L-seryl-L-valyl-L-prolyl-L-asparaginyl-L-prolyl-L-leucylglycyl-L-phenylalanyl-L-phenylalanyl-L-prolyl-L-α-aspartyl-L-histidyl-L-glutaminyl-L-leucyl-L-α-aspartyl-L-prolyl-L-alanyl-L-phenylalanylglycyl-L-alanyl-L-asparaginyl-L-seryl-L-asparaginyl-L-asparaginyl-L-prolyl-L-α-aspartyl-L-tryptophyl-L-α-aspartyl-L-phenylalanyl-L-asparaginyl-L-prolyl-L-asparaginyl-L-lysyl-L-α-aspartyl-L-histidyl-L-tryptophyl-L-prolyl-L-α-glutamyl-L-alanyl-L-asparaginyl-L-lysyl-L-valylglycinamide
bulévirtide	*N*-tétradécanoylglycyl-L-thréonyl-L-asparaginyl-L-leucyl-L-séryl-L-valyl-L-prolyl-L-asparaginyl-L-prolyl-L-leucylglycyl-L-phénylalanyl-L-phénylalanyl-L-prolyl-L-α-aspartyl-L-histidyl-L-glutaminyl-L-leucyl-L-α-aspartyl-L-prolyl-L-alanyl-L-phénylalanylglycyl-L-alanyl-L-asparaginyl-L-séryl-L-asparaginyl-L-asparaginyl-L-prolyl-L-α-aspartyl-L-tryptophyl-L-α-aspartyl-L-phénylalanyl-L-asparaginyl-L-prolyl-L-asparaginyl-L-lysyl-L-α-aspartyl-L-histidyl-L-tryptophyl-L-prolyl-L-α-glutamyl-L-alanyl-L-asparaginyl-L-lysyl-L-valylglycinamide

bulevirtida

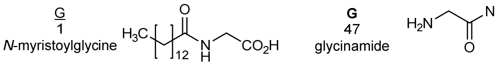
N-tetradecanoilglicil-L-treonil-L-asparaginil-L-leucil-L-seril-L-valil-L-prolil-L-asparaginil-L-prolil-L-leucilglicil-L-fenilalanil-L-fenilalanil-L-prolil-L-α-aspartil-L-histidil-L-glutaminil-L-leucil-L-α-aspartil-L-prolil-L-alanil-L-fenilalanilglicil-L-alanil-L-asparaginil-L-seril-L-asparaginil-L-asparaginil-L-prolil-L-α-aspartil-L-triptofil-L-α-aspartil-L-fenilalanil-L-asparaginil-L-prolil-L-asparaginil-L-lisil-L-α-aspartil-L-histidil-L-triptofil-L-prolil-L-α-glutamil-L-alanil-L-asparaginil-L-lisil-L-valilglicinamida

$C_{248}H_{355}N_{65}O_{72}$

Sequence / Séquence / Secuencia

```
GTNLSVPNPL GFFPDHQLDP AFGANSNNPD WDFNPNKDHW PEANKVG      47
```

Modified residues / Résidus modifiés / Restos modificados



cedazuridinum

cedazuridine

(4*R*)-1-(2-deoxy-2,2-difluoro-β-D-*erythro*-pentofuranosyl)-4-hydroxy-1,3-diazinan-2-one

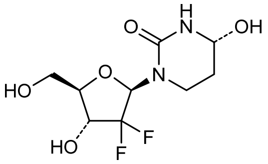
cédazuridine

(4*R*)-1-(2-désoxy-2,2-difluoro-β-D-*érythro*-pentofuranosyl)-4-hydroxy-1,3-diazinan-2-one

cedazuridina

(4*R*)-1-(2-desoxi-2,2-difluoro-β-D-*eritro*-pentofuranosil)-4-hidroxi-1,3-diazinan-2-ona

$C_9H_{14}F_2N_2O_5$



cetrelimabum #

cetrelimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* PDCD1 (programmed cell death 1, PD-1, PD1, CD279)], human monoclonal antibody;
gamma4 heavy chain (1-450) [*Homo sapiens* VH (IGHV1-69*01 (99.0%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG4*01 (CH1 (124-221), hinge S10>P (231) (222-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (124-450)], (137-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-11*01 (96.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimer (229-229'':232-232'')-bisdisulfide

cétrélimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* PDCD1 (protéine 1 de mort cellulaire programmée, PD-1, PD1, CD279)], anticorps monoclonal humain;

chaîne lourde gamma4 (1-450) [*Homo sapiens* VH (IGHV1-69*01 (99.0%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG4*01 (CH1 (124-221), charnière S10>P (231) (222-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (124-450)], (137-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-11*01 (96.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure

cetrelimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* PDCD1 (proteína 1 de muerte celular programada, PD-1, PD1, CD279)], anticuerpo monoclonal humanizado;
cadena pesada gamma4 (1-450) [*Homo sapiens* VH (IGHV1-69*01 (99.0%) -(IGHD) -IGHJ4*01 (92.9%)) [8.8.16] (1-123) -*Homo sapiens* IGHG4*01 (CH1 (124-221), bisagra S10>P (231) (222-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (124-450)], (137-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV3-11*01 (96.8%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG  50
IIPIFDTANY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARPG 100
LAAAYDTGSL DYWGQGTLVT VSSASTKGPS VFPLAPCSRS TSESTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TKTYTCNVDH KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ 350
VYTLPPSQEE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPAT LSLSPGERAT LSCRASQSVR SYLAWYQQKP GQAPRLLIYD  50
ASNRATGIPA RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ RNYWPLTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

```
Intra-H (C23-C104)   22-96     150-206    264-324    370-428
                     22"-96"   150"-206"  264"-324"  370"-428"
Intra-L (C23-C104)   23'-88'   134'-194'
                     23'"-88'"  134'"-194'"
Inter-H-L (CH1 10-CL 126)   137-214'   137"-214'"
Inter-H-H (h 8, h 11)       229-229"   232-232"
```

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

cevidoplenibum

cevidoplenib

(1^{4}*S*)-1^{4}-hydroxy-3^{3},6^{1}-dimethyl-6^{1}*H*-5-aza-6(5,3)-indola-4(4,2)-pyrimidina-1(2)-[1,2]oxazolidina-3(4,1)-pyrazola-8(1)-cyclopropanaoctaphan-7-one

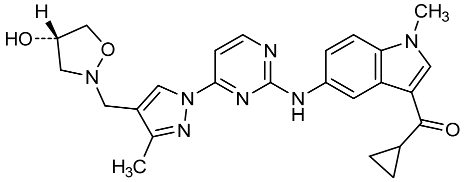
cévidoplénib

(1^{4}*S*)-1^{4}-hydroxy-3^{3},6^{1}-diméthyl-6^{1}*H*-5-aza-6(5,3)-indola-4(4,2)-pyrimidina-1(2)-[1,2]oxazolidina-3(4,1)-pyrazola-8(1)-cyclopropanaoctaphan-7-one

cevidoplenib

(1^{4}*S*)-1^{4}-hidroxi-3^{3},6^{1}-dimetil-6^{1}*H*-5-aza-6(5,3)-indola-4(4,2)-pirimidina-1(2)-[1,2]oxazolidina-3(4,1)-pirazola-8(1)-ciclopropanaoctafan-7-ona

$C_{25}H_{27}N_7O_3$



cibisatamabum #

cibisatamab

immunoglobulin G1-kappa/lambda with domain crossover, anti-[*Homo sapiens* CEACAM5 (carcinoembryonic antigen-related cell adhesion molecule 5, CEA, CD66e)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], humanized monoclonal antibody, bispecific, trivalent;
gamma-kappa heavy chain anti-CEACAM5 and anti-CD3E (VH-CH1-VH-C-kappa-CH2-CH3) (1-694) [humanized VH anti-CEACAM5 (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), hinge 1-6 (220-225)) (122-225) -10-mer bis(tetraglycyl-seryl) linker (226-235) -humanized VH anti-CD3E (*Homo sapiens* IGHV3-23*03 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (236-360) -*Homo sapiens* IGKC*01, R1.4>S (361), Km3 A45.1 (406), V101 (444) (361-467) -*Homo sapiens* IGHG1*01, G1m1 (hinge 5-15 (467-477), CH2 [L1.3>A (481), L1.2>A (482), P114>G (576)] (478-587), CH3 D12 (603), L14 (605) [S10>C (601), T22>W (613)] (588-692), CHS (693-694)) (468-694)]; (224-215''')-disulfide with kappa light chain anti-CEACAM5 (1'''-215''') [humanized V-KAPPA (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'''-108''') -*Homo sapiens* IGKC*01 Km3 A45.1 (154), V101 (192) (109'''-215''')]; (467-214')-disulfide with lambda-gamma light chain anti-CD3E (1'-214') [V-LAMBDA (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (80%) -IGLJ3*01 (100%)) [9.3.9] (1'-109') -2-mer biseryl linker (110'-111') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (208) (112'-209') -hinge 1-5 (210'-214'))]; gamma1 heavy chain anti-CEACAM5 (1''-451'') [humanized VH (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1''-121'') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), hinge 1-15 (220-234), CH2 [L1.3>A (238), L1.2>A (239), P114>G (333)] (235-344), CH3 [Y5>C (353), T22>S (370), L24>A (372), Y86>V (411)] (345-449), CHS (450-451)) (122''-451'')]; (224''-215''')-disulfide with kappa light chain anti-CEACAM5 (1'''-215''') [humanized V-KAPPA (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'''-108''') -*Homo sapiens* IGKC*01 Km3 A45.1 (154), V101 (192) (109'''-215''')]; dimer (473-230'':476-233'':601-353'')-trisdisulfide

cibisatamab

immunoglobuline G1-kappa/lambda avec domaines échangés, anti-[*Homo sapiens* CEACAM5 (molécule d'adhésion cellulaire 5 apparentée à l'antigène carcinoembryonaire, CEA, CD66e)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)], anticorps monoclonal humanisé, bispécifique, trivalent;

chaîne lourde gamma-kappa anti-CEACAM5 et anti-CD3E (VH-CH1-VH-C-kappa-CH2-CH3) (1-694) [VH anti-CEACAM5 humanisé (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), charnière 1-6 (220-225)) (122-225) -10-mer bis(tétraglycyl-séryl) linker (226-235) -VH anti-CD3E humanisé (*Homo sapiens* IGHV3-23*03 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (236-360) -*Homo sapiens* IGKC*01, R1.4>S (361), Km3 A45.1 (406), V101 (444) (361-467) -*Homo sapiens* IGHG1*01, G1m1 (charnière 5-15 (467-477), CH2 [L1.3>A (481), L1.2>A (482), P114>G (576)] (478-587), CH3 D12 (603), L14 (605) [S10>C (601), T22>W (613)] (588-692), CHS (693-694)) (468-694)]; (224-215''')-disulfure avec la chaîne légère kappa anti-CEACAM5 (1'''-215''') (V-KAPPA humanisé (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'''-108''') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'''-215''')]; (467-214')-disulfure avec la chaîne légère lambda-gamma anti-CD3E (1'-214') [V-LAMBDA (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (80%) -IGLJ3*01 (100%)) [9.3.9] (1'-109') -2-mer biséryl linker (110'-111') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (208) (112'-209') -charnière 1-5 (210'-214'))];
chaîne lourde gamma1 anti-CEACAM5 (1''-451'') [VH humanisé (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1''-121'') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), charnière 1-15 (220-234), CH2 [L1.3>A (238), L1.2>A (239), P114>G (333)] (235-344), CH3 [Y5>C (353), T22>S (370), L24>A (372), Y86>V (411)] (345-449), CHS (450-451)) (122''-451'')]; (224''-215''')-disulfure avec la chaîne légère kappa anti-CEACAM5 (1'''-215''') [V-KAPPA humanisé (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'''-108''') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'''-215''')]; dimère (473-230'':476-233'':601-353'')-trisdisulfure

cibisatamab

inmunoglobulina G1-kappa/lambda con dominios intercambiados, anti-[*Homo sapiens* CEACAM5 (molécula de adhesión celular 5 relacionada con el antígeno carcinoembrionario, CEA, CD66e)] y anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)], anticuerpo monoclonal humanizado, biespecífico, trivalente;
cadena pesada gamma-kappa anti-CEACAM5 y anti-CD3E (VH-CH1-VH-C-kappa-CH2-CH3) (1-694) [VH anti-CEACAM5 humanizado (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1-121) -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), bisagra 1-6 (220-225)) (122-225) -10-mer bis(tetraglicil-seril) ligando (226-235) -VH anti-CD3E humanizado (*Homo sapiens* IGHV3-23*03 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (236-360) -*Homo sapiens* IGKC*01, R1.4>S (361), Km3 A45.1 (406), V101 (444) (361-467) -*Homo sapiens* IGHG1*01, G1m1 (bisagra 5-15 (467-477), CH2 [L1.3>A (481), L1.2>A (482), P114>G (576)] (478-587), CH3 D12 (603), L14 (605) [S10>C (601), T22>W (613)] (588-692), CHS (693-694)) (468-694)]; (224-215''')-disulfuro con la cadena ligera kappa anti-CEACAM5 (1'''-215''') (V-KAPPA humanizado (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'''-108''') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'''-215''')]; (467-214')-disulfuro con la cadena ligera lambda-gamma anti-CD3E (1'-214') [V-LAMBDA (*Mus musculus* IGLV1*01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46*01 (80%) -IGLJ3*01 (100%)) [9.3.9] (1'-109') -2-mer biseril ligando (110'-111') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (208) (112'-209') -bisagra 1-5 (210'-214'))];
cadena pesada gamma1 anti-CEACAM5 (1''-451'') [VH humanizado (*Homo sapiens* IGHV1-18*01 (82.7%) -(IGHD) -IGHJ4*01 (92.3%)) [8.8.14] (1''-121'') -*Homo sapiens* IGHG1*01, G1m17 (CH1 K120 (218) (122-219), bisagra 1-15 (220-234), CH2 [L1.3>A (238), L1.2>A (239), P114>G (333)] (235-344), CH3 [Y5>C (353), T22>S (370), L24>A (372), Y86>V (411)] (345-449), CHS (450-451)) (122''-451'')]; (224''-215''')-disulfuro con la cadena ligera kappa anti-CEACAM5 (1'''-215''') [V-KAPPA humanizado (*Homo sapiens* IGKV1-16*01 (82.1%) -IGKJ2*02 (100%)) [6.3.10] (1'''-108''') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'''-215''')]; dímero (473-230'':476-233'':601-353'')-trisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada anti-CEACAM5 and anti-CD3E

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT EFGMNWVRQA PGQGLEWMGW  50
INTKTGEATY VEEFKGRVTF TTDTSTSTAY MELRSLRSDD TAVYYCARWD 100
FAYYVEAMDY WGQGTTVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDGGGGS GGGGSEVQLL ESGGGLVQPG 250
GSLRLSCAAS GFTFSTYAMN WVRQAPGKGL EWVSRIRSKY NNYATYYADS 300
VKGRFTISRD DSKNTLYLQM NSLRAEDTAV YYCVRHGNFG NSYVSWFAYW 350
GQGTLVTVSS ASVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ 400
WKVDNALQSG NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT 450
HQGLSSPVTK SFNRGECDKT HTCPPCPAPE AAGGPSVFLF PPKPKDTLMI 500
SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV 550
SVLTVLHQDW LNGKEYKCKV SNKALGAPIE KTISKAKGQP REPQVYTLPP 600
CRDELTKNQV SLWCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS 650
FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK       694
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Light chain / Chaîne légère / Cadena ligera anti-CD3E

```
QAVVTQEPSL TVSPGGTVTL TCGSSTGAVT TSNYANWVQE KPGQAFRGLI  50
GGTNKRAPGT PARFSGSLLG GKAALTLSGA QPEDEAEYYC ALWYSNLWVF 100
GGGTKLTVLS SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV 150
SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP 200
SNTKVDKKVE PKSC                                       214
```

Heavy chain / Chaîne lourde / Cadena pesada anti-CEACAM5

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT EFGMNWVRQA PGQGLEWMGW  50
INTKTGEATY VEEFKGRVTF TTDTSTSTAY MELRSLRSDD TAVYYCARWD 100
FAYYVEAMDY WGQGTTVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPEAAG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALGAPIEKTI SKAKGQPREP 350
QVCTLPPSRD ELTKNQVSLS CAVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL VSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                     451
```

Light chain / Chaîne légère / Cadena ligera anti-CEACAM5

```
DIQMTQSPSS LSASVGDRVT ITCKASAAVG TYVAWYQQKP GKAPKLLIYS  50
ASYRKRGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCHQ YYTYPLFTFG 100
QGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                      215
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

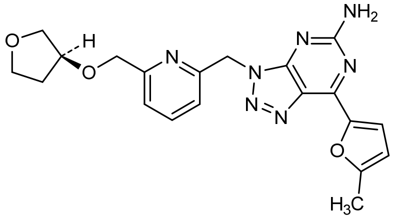
```
Intra-H (C23-C104)  22-96    148-204    257-333    387-447  508-568  614-672
                    22''-96''  148''-204''  265''-325''  371''-429''
Intra-L (C23-C104)  22'-90'    138'-194'
                    23'''-88'''  135'''-195'''
Inter-H-L (h 5-CL 126)          224-215'''  467-214'  224''-215'''
Inter-H-H (h 11, h 14, AA >C)   473-230''   476-233''  601-353''
```

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
544, 301''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

ciforadenantum

ciforadenant	(7^3*S*)-1^5-methyl-6-oxa-2(7,3)-[1,2,3]triazolo[4,5-*d*]pyrimidina-4(2,6)-pyridina-1(2)-furana-7(3)-oxolanaheptaphan-2^5-amine
ciforadénant	(7^3*S*)-1^5-méthyl-6-oxa-2(7,3)-[1,2,3]triazolo[4,5-*d*]pyrimidina-4(2,6)-pyridina-1(2)-furana-7(3)-oxolanaheptaphan-2^5-amine
ciforadenant	(7^3*S*)-1^5-metil-6-oxa-2(7,3)-[1,2,3]triazol[4,5-*d*]pirimidina-4(2,6)-piridina-1(2)-furana-7(3)-oxolanaheptafan-2^5-amina

$C_{20}H_{21}N_7O_3$



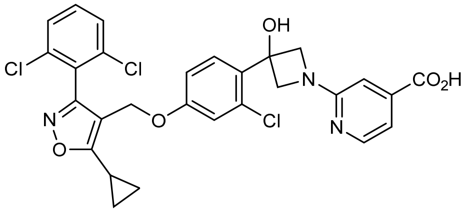
cilofexorum

cilofexor $3^2,7^2,7^6$-trichloro-6^5-cyclopropyl-2^3-hydroxy-4-oxa-1(2)-pyridina-6(4,3)-[1,2]oxazola-2(1,3)-azetidina-3(1,4),7(1)-dibenzenaheptaphane-1^4-carboxylic acid

cilofexor acide $3^2,7^2,7^6$-trichloro-6^5-cyclopropyl-2^3-hydroxy-4-oxa-1(2)-pyridina-6(4,3)-[1,2]oxazola-2(1,3)-azétidina-3(1,4),7(1)-dibenzenaheptaphane-1^4-carboxylique

cilofexor ácido $3^2,7^2,7^6$-tricloro-6^5-ciclopropil-2^3-hidroxi-4-oxa-1(2)-piridina-6(4,3)-[1,2]oxazola-2(1,3)-azetidina-3(1,4),7(1)-dibencenaheptafano-1^4-carboxílico

$C_{28}H_{22}Cl_3N_3O_5$



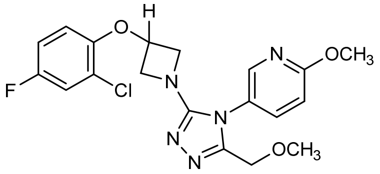
cligosibanum

cligosiban 5-{3-[3-(2-chloro-4-fluorophenoxy)azetidin-1-yl]-5-(methoxymethyl)-4*H*-1,2,4-triazol-4-yl}-2-methoxypyridine

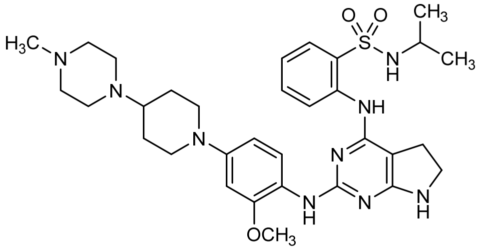
cligosiban 5-{3-[3-(2-chloro-4-fluorophénoxy)azétidin-1-yl]-5-(méthoxyméthyl)-4*H*-1,2,4-triazol-4-yl}-2-méthoxypyridine

cligosibán 5-{3-[3-(2-cloro-4-fluorofenoxi)azetidin-1-il]-5-(metoximetil)-4*H*-1,2,4-triazol-4-il}-2-metoxipiridina

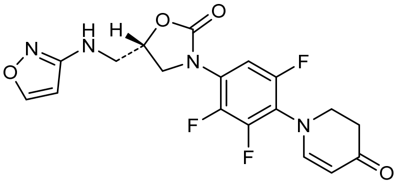
$C_{19}H_{19}ClFN_5O_3$



conteltinibum

conteltinib	2-[(2-{2-methoxy-4-[4-(4-methylpiperazin-1-yl)piperidin-1-yl]anilino}-6,7-dihydro-5*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)amino]-*N*-(propan-2-yl)benzene-1-sulfonamide
conteltinib	2-[(2-{2-méthoxy-4-[4-(4-méthylpipérazin-1-yl)pipéridin-1-yl]anilino}-6,7-dihydro-5*H*-pyrrolo[2,3-*d*]pyrimidin-4-yl)amino]-*N*-(propan-2-yl)benzène-1-sulfonamide
conteltinib	2-[(2-{2-metoxi-4-[4-(4-metilpiperazin-1-il)piperidin-1-il]anilino}-6,7-dihidro-5*H*-pirrolo[2,3-*d*]pirimidin-4-il)amino]-*N*-(propan-2-il)benceno-1-sulfonamida
	$C_{32}H_{45}N_9O_3S$
	

contezolidum

contezolid	1-{2,3,6-trifluoro-4-[(5S)-5-{[(1,2-oxazol-3-yl)amino]methyl}-2-oxo-1,3-oxazolidin-3-yl]phenyl}-2,3-dihydropyridin-4(1*H*)-one
contézolid	1-(2,3,6-trifluoro-4-{(5*S*)-5-[(1,2-oxazol-3-ylamino)méthyl]-2-oxo-1,3-oxazolidin-3-yl}phényl)-2,3-dihydropyridin-4(1*H*)-one
contezolid	1-(2,3,6-trifluoro-4-{(5*S*)-5-[(1,2-oxazol-3-ilamino)metil]-2-oxo-1,3-oxazolidin-3-il}fenil)-2,3-dihidropiridin-4(1*H*)-ona
	$C_{18}H_{15}F_3N_4O_4$
	

cusatuzumabum #

cusatuzumab	immunoglobulin G1-lambda, anti-[*Homo sapiens* CD70 (tumor necrosis factor superfamily member 7, TNFSF7, CD27LG, CD27L)], humanized monoclonal antibody; gamma1 heavy chain (1-452) [humanized VH (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD)-IGHJ5*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (219) (123-220), hinge (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfide with lambda light chain (1'-216') [humanized V-LAMBDA (*Homo sapiens* IGLV8-61*01 (78.1%) -IGLJ7*01 (100%)) [9.3.10] (1'-110') -*Homo sapiens* IGLC2*01 (111'-216')]; dimer (231-231":234-234")-bisdisulfide

cusatuzumab	immunoglobuline G1-lambda, anti-[*Homo sapiens* CD70 (membre 7 de la superfamille du facteur de nécrose tumorale (TNF), TNFSF7, CD27LG, CD27L)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-452) [VH humanisé (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD)-IGHJ5*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (219) (123-220), charnière (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfure avec la chaîne légère lambda (1'-216') [V-LAMBDA humanisé (*Homo sapiens* IGLV8-61*01 (78.1%) -IGLJ7*01 (100%)) [9.3.10] (1'-110') -*Homo sapiens* IGLC2*01 (111'-216')]; dimère (231-231":234-234")-bisdisulfure
cusatuzumab	inmunoglobulina G1-lambda, anti-[*Homo sapiens* CD70 (miembro 7 de la superfamilia del factor de necrosis tumoral (TNF), TNFSF7, CD27LG, CD27L)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-452) [VH humanizado (*Homo sapiens* IGHV3-48*03 (90.8%) -(IGHD)-IGHJ5*01 (100%)) [8.8.15] (1-122) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (219) (123-220), bisagra (221-235), CH2 (236-345), CH3 D12 (361), L14 (363) (346-450), CHS (451-452)) (123-452)], (225-215')-disulfuro con la cadena ligera lambda (1'-216') [V-LAMBDA humanizado (*Homo sapiens* IGLV8-61*01 (78.1%) -IGLJ7*01 (100%)) [9.3.10] (1'-110') -*Homo sapiens* IGLC2*01 (111'-216')]; dímero (231-231":234-234")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS VYYMNWVRQA PGKGLEWVSD  50
INNEGGTTYY ADSVKGRFTI SRDNSKNSLY LQMNSLRAED TAVYYCARDA 100
GYSNHVPIFD SWGQGTLVTV SSASTKGPSV FPLAPSSKST SGGTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELL GGPSVFLFPP 250
KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE 350
PQVYTLPPSR DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP 400
PVLDSDGSFF LYSKLTVDKS RWQQGNVFSC SVMHEALHNH YTQKSLSLSP 450
GK                                                    452
```

Light chain / Chaîne légère / Cadena ligera

```
QAVVTQEPSL TVSPGGTVTL TCGLKSGSVT SDNFPTWYQQ TPGQAPRLLI  50
YNTNTRHSGV PDRFSGSILG NKAALTITGA QADDEAEYFC ALFISNPSVE 100
FGGGTQLTVL GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV 150
AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHRSYSCQVT 200
HEGSTVEKTV APTECS                                     216
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	149-205	266-326	372-430
	22"-96"	149"-205"	266"-326"	372"-430"
Intra-L (C23-C104)	22'-90'	138'-197'		
	22'''-90'''	138'''-197'''		
Inter-H-L (h 5-CL 126)	225-215'	225"-215'''		
Inter-H-H (h 11, h 14)	231-231"	234-234"		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
302, 302"

Afucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes afucosylés / glicanos de tipo CHO biantenarios complejos afucosilados

dalcinonacogum alfa #

dalcinonacog alfa	human blood coagulation factor IX variant (R318Y, R338E, T343R), produced in Chinese hamster ovary (CHO) cells, glycoform alfa.
dalcinonacog alfa	variant (R318Y, R338E, T343R) du facteur de coagulation sanguine IX humain, produit par des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa
dalcinonacog alfa	variante (R318Y, R338E, T343R) del factor de coagulación sanguínea IX humano, producido por las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
YNSGKLEEFV QGNLERECME EKCSFEEARE VFENTERTTE FWKQYVDGDQ   50
CESNPCLNGG SCKDDINSYE CWCPFGFEGK NCELDVTCNI KNGRCEQFCK  100
NSADNKVVCS CTEGYRLAEN QKSCEPAVPF PCGRVSVSQT SKLTRAETVF  150
PDVDYVNSTE AETILDNITQ STQSFNDFTR VVGGEDAKPG QFPWQVVLNG  200
KVDAFCGGSI VNEKWIVTAA HCVETGVKIT VVAGEHNIEE TEHTEQKRNV  250
IRIIPHHNYN AAINKYNHDI ALLELDEPLV LNSYVTPICI ADKEYTNIFL  300
KFGSGYVSGW GRVFHKGYSA LVLQYLRVPL VDRATCLEST KFRIYNNMFC  350
AGFHEGGRDS CQGDSGGPHV TEVEGTSFLT GIISWGEECA MKGKYGIYTK  400
VSRYVNWIKE KTKLT                                        415
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
18-23 51-62 56-71 73-82 88-99 95-109
111-124 132-289 206-222 336-350 361-389
Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)
Asn-157 Asn-167
Glycosylation sites (O) / Sites de glycosylation (O) / Posiciones de glicosilación (O)
Ser-53 Ser-61 Thr-159 Thr-169 Thr-172 Thr-179
Non-conventional residues / Résidus non conventionnels / Restos no convencionales
Tyr-318 Glu-338 Arg-343

delolimogenum mupadenorepvecum #

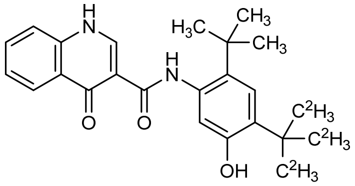
delolimogene mupadenorepvec	a conditionally replicating adenovirus serotype 5/35 genetically engineered to express a trimerized membrane-bound CD40 ligand (TMZ-CD40L) and tumor necrosis factor superfamily member 9 (TNFSF9, 4-1BBL, CD137), under the control of a cytomegalovirus (CMV) promoter, and with deletions in E1A gene and E3 genes.
délolimogène mupadénorépvec	adénovirus de sérotype 5/35 dont la réplication est conditionnée, génétiquement modifié pour exprimer le ligand membranaire du récepteur CD40 (TMZ-CD40L) sous forme trimérique et le membre 9 de la superfamille du facteur de nécrose tumorale (TNFSF9, 4-1BBL, CD137), sous le contrôle d'un promoteur du cytomégalovirus (CMV) et avec des délétions sur le gène E1A et les gènes E3
delolimogén mupadenorepvec	un adenovirus de serotipo 5/35 con replicación condicionada, modificado genéticamente para expresar un ligando de membrana trimerizado de CD40 (TMZ-CD40L) y el miembro 9 de la superfamilia de factores de necrosis tumoral (TNFSF9, 4-1BBL, CD137), bajo el control de un promotor del citomegalovirus (CMV) y con deleciones en el gen E1A y en los genes E3

deutivacaftorum

deutivacaftor	*N*-{2-*tert*-butyl-5-hydroxy-4-[2-($^{2}H_3$)methyl(1,1,1,3,3,3-$^{2}H_6$)propan-2-yl]phenyl}-4-oxo-1,4-dihydroquinoline-3-carboxamide

deutivacaftor	*N*-{2-*tert*-butyl-5-hydroxy-4-[2-($^{2}H_{3}$)méthyl(1,1,1,3,3,3-$^{2}H_{6}$)propan-2-yl]phényl}-4-oxo-1,4-dihydroquinoline-3-carboxamide
deutivacaftor	*N*-{2-*tert*-butil-5-hidroxi-4-[2-($^{2}H_{3}$)metil(1,1,1,3,3,3-$^{2}H_{6}$)propan-2-il]fenil}-4-oxo-1,4-dihidroquinolina-3-carboxamida

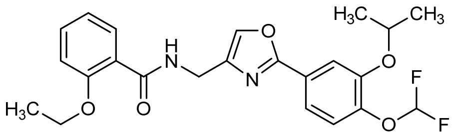
$C_{24}H_{19}{}^{2}H_{9}N_{2}O_{3}$



difamilastum

difamilast	*N*-({2-[4-(difluoromethoxy)-3-(propan-2-yloxy)phenyl]-1,3-oxazol-4-yl}methyl)-2-ethoxybenzamide
difamilast	*N*-({2-[4-(difluorométhoxy)-3-(propan-2-yloxy)phényl]-1,3-oxazol-4-yl}méthyl)-2-éthoxybenzamide
difamilast	*N*-({2-[4-(difluorometoxi)-3-(propan-2-iloxi)fenil]-1,3-oxazol-4-il}metil)-2-etoxibenzamida

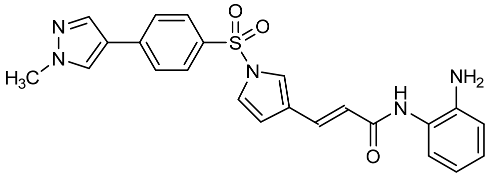
$C_{23}H_{24}F_{2}N_{2}O_{5}$

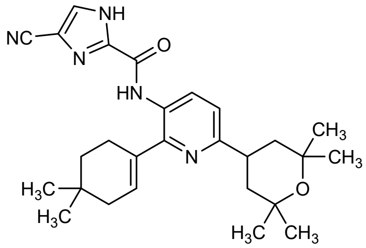


domatinostatum

domatinostat	(2*E*)-*N*-(2-aminophenyl)-3-(1-{[4-(1-methyl-1*H*-pyrazol-4-yl)phenyl]sulfonyl}-1*H*-pyrrol-3-yl)prop-2-enamide
domatinostat	(2*E*)-*N*-(2-aminophényl)-3-(1-{[4-(1-méthyl-1*H*-pyrazol-4-yl)phényl]sulfonyl}-1*H*-pyrrol-3-yl)prop-2-énamide
domatinostat	(2*E*)-*N*-(2-aminofenil)-3-(1-{[4-(1-metil-1*H*-pirazol-4-il)fenil]sulfonil}-1*H*-pirrol-3-il)prop-2-enamida

$C_{23}H_{21}N_{5}O_{3}S$



edicotinibum	
edicotinib	4-cyano-*N*-[2-(4,4-dimethylcyclohex-1-en-1-yl)-6-(2,2,6,6-tetramethyloxan-4-yl)pyridin-3-yl]-1*H*-imidazole-2-carboxamide
édicotinib	4-cyano-*N*-[2-(4,4-diméthylcyclohex-1-én-1-yl)-6-(2,2,6,6-tétraméthyloxan-4-yl)pyridin-3-yl]-1*H*-imidazole-2-carboxamide
edicotinib	4-ciano-*N*-[2-(4,4-dimetilciclohex-1-en-1-il)-6-(2,2,6,6-tetrametiloxan-4-il)piridin-3-il]-1*H*-imidazol-2-carboxamida
	$C_{27}H_{35}N_5O_2$
	

efavaleukinum alfa #	
efavaleukin alfa	immunoglobulin G1 γ1-chain C-terminal constant region fragment (Fc) (1-226 without C-terminal Lys, N77G,D136E,L138M variant)-G_4S linker (227-231)-human interleukin 2 (232-364, V322K,C356A variant) fusion protein, dimer disulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
éfavaleukine alfa	région constante C-terminale de la chaîne γ1 de l'immunoglobuline G1 humaine (fragment Fc) (1-226 sans la lysine C-terminale, variant N77G,D136E,L138M)-linker G_4S (227-231)-interleukine 2 humaine (232-364, variant V322K, C356A), protéine de fusion, dimère disulfure, produite par des cellules de hamsters chinois (CHO), glycoforme alfa
efavaleukina alfa	región constante C-terminal de la cadena γ1 de la inmunoglobulina G1 humana (fragmento Fc) (1-226 sin la lisina C-terminal, variante N77G,D136E,L138M)-ligante G_4S (227-231)-interleukina 2 humana (232-364, variante V322K, C356A), proteína de fusión, dímero disulfuro, producido por las células de hamsters chinos (CHO), glicoforma alfa

```
DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED 50
PEVKFNWYVD GVEVHNAKTK PREEQYGSTY RVVSVLTVLH QDWLNGKEYK 100
CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK 150
GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 200
NVFSCSVMHE ALHNHYTQKS LSLSPGGGGG SAPTSSSTKK TQLQLEHLLL 250
DLQMILNGIN NYKNPKLTRM LTFKFYMPKK ATELKHLQCL EEELKPLEEV 300
LNLAQSKNFH LRPRDLISNI NKIVLELKGS ETTFMCEYAD ETATIVEFLN 350
RWITFAQSII STLT                                        364
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
intra-chain: 41-101 147-205 289-336
41'-101' 147'-205' 289'-336'
inter-chain: 6-6' 9-9'

Glycosylation site (O) / Site de glycosylation (O) / Posición de glicosilación (O)
Thr-234 Thr-234'

efineptakinum alfa	
efineptakin alfa	Met-Gly-Met (1-3)-human interleukin 7 (4-155) fused to an antibody hybrid fragment (hyFc) consisting of human immunoglobulin D (IgD) hinge and N-terminal CH2 regions (156-193) and human immunoglobulin G4 (IgG4) C-terminal CH2 and complete CH3 regions (194-400), dimer disulfide, produced in Chinese hamster ovary (CHO) cells, glycoform alfa
éfineptakine alfa	Met-Gly-Met (1-3)-interleukine 7 humaine (4-155), fusionnée à un fragment Fc hybride d'anticorps (hyFc) consistant en la région charnière et le domaine CH2 N-terminal de l'immunoglobuline D (IgD) humaine (156-193), fusionné au domaine CH2 C-terminal et au domaine complet CH3 de l'immunoglobuline G4 (IgG4) humaine (194-400), dimère disulfure, produit par des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa
efineptakina alfa	Met-Gly-Met (1-3)-interleukina 7 humana (4-155), fusionada con un fragmento Fc híbrido del anticuerpo (hyFc) consistente en la región bisagra y el dominio CH2 N-terminal de la inmunoglobulina D (IgD) humana (156-193), fusionada con el dominio CH2 C-terminal y con el dominio completo CH3 de la inmunoglobulina G4 (IgG4) humana (194-400), dímero disulfuro, producido por las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
MGMDCDIEGK DGKQYESVLM VSIDQLLDSM KEIGSNCLNN EFNFFKRHIC 50
DANKEGMFLF RAARKLRQFL KMNSTGDFDL HLLKVSEGTT ILLNCTGQVK 100
GRKPAALGEA QPTKSLEENK SLKEQKKLND LCFLKRLLQE IKTCWNKILM 150
GTKEHRNTGR GGEEKKKEKE KEEQEERETK TPECPSHTQP LGVFLFPPKP 200
KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN 250
STYRVVSVLT VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ 300
VYTLPPSQEE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 350
LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV MHEALHNHYT QKSLSLSLGK 400
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 5-95 37-132 50-144 214-274 320-378
5'-95' 37'-132' 50'-144' 214'-274' 320'-378'
Inter-chain: 184-184'

Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)
Asn-73 Asn-94 Asn-250
Glycosylation site (O) / Site de glycosylation (O) / Posición de glicosilación (O)
Thr-113

efinopegdutidum #	
efinopegdutide	oxyntomodulin analogue, conjugated by a 10 kDa polyethylene glycol (PEG) linker (n ~ 225) to an Fc portion dimer of human immunoglobulin G4 (IgG4): $N^{1.1}$-{3-[α-(3-{3-[(3*RS*)-3-({16,20-anhydro-[Ser^{2}>Aib,Ser^{16}>Glu,Arg^{17}>Lys,Gln^{20}>Lys,Asp^{21}>Glu,Lys^{30}> Cys]-oxyntomodulin (1-30)-peptide 30-amide}-$S^{3.30}$-yl)-2,5-dioxopyrrolidin-1-yl]propanamido}propyl) poly(oxyethylene)-ω-yloxy]propyl}[immunoglobulin G4 heavy chain constant region C-terminal 221-peptide dimer disulfide], non-glycosylated, immunoglobulin fragment dimer produced in *Escherichia coli*
éfinopégdutide	analogue de l' oxyntomoduline, conjugué par un linker polyéthylène glycol (PEG) de 10 kDa (n ~ 225) à un dimère de fragment Fc d'immunoglobuline G4 (IgG4) humaine: $N^{1.1}$-{3-[α-(3-{3-[(3*RS*)-3-({16,20-anhydro-[Ser^{2}>Aib,Ser^{16}>Glu,Arg^{17}>Lys,Gln^{20}>Lys,Asp^{21}>Glu,Lys^{30}> Cys]-oxyntomodulin

(1-30)-peptide 30-amide}-*S*$^{3.30}$-yl)-2,5-dioxopyrrolidin-1-yl]propanamido}propyl) poly(oxyéthylène)-ω-yloxy]propyl}[peptide de 221 acides aminés de la région constante C-terminale de la chaîne lourde G4 d'immunoglobuline, dimère disulfure], non-glycosylé, dimère du fragment d'immunoglobuline produit par *Escherichia coli*

efinopegdutida

análogo de la oxintomodulina, conjugado por un enlace polietileno glicol (PEG) de 10 kDa (n ~ 225) a un dímero del fragmento Fc de la inmunoglobulina G4 (IgG4) humana:
N$^{1.1}$-{3-[α-(3-{3-[(3*RS*)-3-({16,20-anhidro-[Ser^{2}>Aib,Ser^{16}>Glu,Arg^{17}>Lys,Gln^{20}>Lys,Asp^{21}>Glu,Lys^{30}> Cys]-oxintomodulin
(1-30)-péptido 30-amida}-*S*$^{3.30}$-il)-2,5-dioxopirrolidin-1-il]propanamido}propil)poli(oxietileno)-ω-iloxi]propil}[péptido de 221 aminoácidos de la región constante C-terminal de la cadena pesada G4 de la inmunoglobulina, dímero disulfuro], no glicosilado, dímero del fragmento de la inmunoglobulina producido por *Escherichia coli*

Conjugated peptide / peptide conjugué / péptido conjugado

```
HBQGTFTSDY SKYLDEKRAK EFVQWLMNTC-NH2
```

Monomer / monomère / monómero IgG4 Fc

```
PSCPAPEFLG GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SQEDPEVQFN 50
WYVDGVEVHN AKTKPREEQF NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK 100
GLPSSIEKTI SKAKGQPREP QVYTLPPSQE EMTKNQVSLT CLVKGFYPSD 150
IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSRLTVDKSR WQEGNVFSCS 200
VMHEALHNHY TQKSLSLSLG K                                221
```

Disulfide bridges location / Positions des ponts disulfure / Posiciones de los puentes disulfuro

Intra-chain: 35-95 141-199 35'-95' 141'-199'

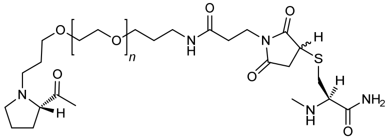
Inter-chain: 3-3'

Modified residues / résidus modifiés / restos modificados

B = 2-methylalanyl (2-aminoisobutyryl, Aib)

E...K = cyclic Glu$^{5.16}$-Lys$^{6.20}$ amide bond

P---C(-NH2) =



eftansomatropinum alfa #

eftansomatropin alfa

human somatotropin (1-191) fused to a hybrid Fc consisting of human immunoglobulin D (IgD) hinge region, fused to the IgD N-terminal CH2 region (192-229), fused to the immunoglobulin G4 (IgG4) C-terminal CH2 region, fused to the IgG4 CH3 region (230-436), disulfide dimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa

eftansomatropine alfa

somatotropine humaine (1-191) fusionnée à un fragment Fc hybride consistant en la région charnière de l'immunoglobuline D (IgD) humaine, fusionnée au domaine CH2 N-terminal de l'IgD (192-229), fusionné au domaine CH2 C-terminal de l'immunoglobuline G4 (IgG4), fusionné au domaine CH3 de l'IgG4 (230-436), dimère disulfure, produit des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa eftansomatropina alfa

somatotropina humana (1-191) fusionada con un fragmento Fc híbrido consistente en la región bisagra de la inmunoglobulina D (IgD) humana, fusionada con el dominio CH2 N-terminal de la IgD (192-229), fusionada con el dominio CH2 C-terminal de la inmunoglobulina G4 (IgG4), fusionada con el dominio CH3 de la IgG4 (230-436), dímero disulfuro, producido en las células ováricas de hamsters chinos (CHO), glicoforma alfa

```
FPTIPLSRLF DNAMLRAHRL HQLAFDTYQE FEEAYIPKEQ KYSFLQNPQT 50
SLCFSESIPT PSNREETQQK SNLELLRISL LLIQSWLEPV QFLRSVFANS 100
LVYGASDSNV YDLLKDLEEG IQTLMGRLED GSPRTGQIFK QTYSKFDTNS 150
HNDDALLKNY GLLYCFRKDM DKVETFLRIV QCRSVEGSCG FRNTGRGGEE 200
KKKEKEKEEQ EERETKTPEC PSHTQPLGVF LFPPKPKDTL MISRTPEVTC 250
VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR VVSVLTVLHQ 300
DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN 350
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT 400
VDKSRWQEGN VFSCSVMHEA LHNHYTQKSL SLSLGK                436
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain : 53-165 182-189 250-310 356-414
53'-165' 182'-189' 250'-310' 356'-414'
Inter-chain : 220-220'

Glycosylation sites (O) / Sites de glycosylation (O) / Posiciones de glicosilación (O)
Ser-55 Ser-57 Thr-60 Ser-62 Thr-67

Glycosylation site (N) / Site de glycosylation (N) / Posición de glicosilación (N)
Asn-286

elismetrepum
elismetrep

4-[(4-cyclopropylisoquinolin-3-yl){[4-(trifluoromethoxy)phenyl]methyl}sulfamoyl]benzoic acid

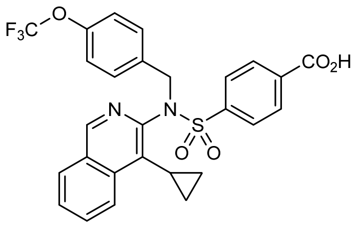
élismétrep

acide 4-[(4-cyclopropylisoquinoléin-3-yl){[4-(trifluorométhoxy)phényl]méthyl}sulfamoyl]benzoïque

elismetrep

ácido 4-[(4-ciclopropilisoquinolein-3-il){[4-(trifluorometoxi)fenil]metil}sulfamoil]benzoico

$C_{27}H_{21}F_3N_2O_5S$



enapotamabum #
enapotamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* AXL (AXL receptor tyrosine kinase, tyrosine-protein kinase receptor UFO)], *Homo sapiens* monoclonal antibody;
gamma1 heavy chain (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.9%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), hinge (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfide with kappa light chain (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (225-225'':228-228'')-bisdisulfide

énapotamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* AXL (récepteur tyrosine kinase AXL, récepteur tyrosine-protéine kinase UFO)], *Homo sapiens* anticorps monoclonal; chaîne lourde gamma1 (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.90%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), charnière (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfure avec la chaîne légère kappa (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (225-225'':228-228'')-bisdisulfure
enapotamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* AXL (receptor tirosina kinasa AXL, receptor tirosina-proteína kinasa UFO)], *Homo sapiens* anticuerpo monoclonal; cadena pesada gamma1 (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.90%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), bisagra (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfuro con la cadena ligera kappa (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (225-225'':228-228'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMNWVRQA PGKGLEWVST  50
TSGSGASTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIW 100
IAFDIWGQGT MVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPG      445
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Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPYTFG 100
QGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                       215
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	143-199	260-320	366-424
	22''-96''	143''-199''	260''-320''	366''-424''
Intra-L (C23-C104)	23'-89'	135'-195'		
	23'''-89'''	135'''-195'''		
Inter-H-L (h 5-CL 126)	219-215'	219''-215'''		
Inter-H-H (h 11, h14)	225-225''	228-228''		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
296, 296''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

enapotamabum vedotinum #

enapotamab vedotin	immunoglobulin G1-kappa, anti-[*Homo sapiens* AXL (AXL receptor tyrosine kinase, tyrosine-protein kinase receptor UFO)], *Homo sapiens* monoclonal antibody conjugated to auristatin E;

gamma1 heavy chain (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.9%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), hinge (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfide with kappa light chain (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (225-225'':228-228'')-bisdisulfide; conjugated, on an average of 4 cysteinyl, to monomethylauristatin E (MMAE), via a cleavable maleimidocaproyl-valyl-citrullinyl-p-aminobenzyloxycarbonyl (mc-val-cit-PABC) type linker
For the *vedotin* part, please refer to the document *"INN for pharmaceutical substances: Names for radicals, groups and others"*.*

énapotamab védotine

immunoglobuline G1-kappa, anti-[*Homo sapiens* AXL (récepteur tyrosine kinase AXL, récepteur tyrosine-protéine kinase UFO)], *Homo sapiens* anticorps monoclonal conjugué à l'auristatine E;
chaîne lourde gamma1 (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.90%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), charnière (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfure avec la chaîne légère kappa (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (225-225'':228-228'')-bisdisulfure; conjugué sur 4 cystéinyl en moyenne, au monométhylauristatine E (MMAE), via un linker clivable de type maléimidocaproyl-valyl-citrullinyl-p-aminobenzyloxycarbonyl (mc-val-cit-PABC)
Pour la partie *védotine*, veuillez-vous référer au document *"INN for pharmaceutical substances: Names for radicals, groups and others"*.*

enapotamab vedotina

inmunoglobulina G1-kappa, anti-[*Homo sapiens* AXL (receptor tirosina kinasa AXL, receptor tirosina-proteína kinasa UFO)], *Homo sapiens* anticuerpo monoclonal conjugado con la auristatina E;
cadena pesada gamma1 (1-445) [*Homo sapiens* VH (IGHV3-23*01 (95.90%) -(IGHD) -IGHJ3*02 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (213) (117-214), bisagra (215-229), CH2 (230-339), CH3 E12 (355), M14 (357) (340-444), CHS K>del (445)) (117-445)], (219-215')-disulfuro con la cadena ligera kappa (1'-215') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (100%) -IGKJ2*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (225-225'':228-228'')-bisdisulfuro; conjugado bajo una media de 4 cisteinil, con la monometilauristatina E (MMAE), a través de un enlace escindible del tipo maliimidocaproil-valil-citrullinil-p-aminobenziloxicarbonil (mc-val-cit-PABC)
Para la fracción *vedotina*, se pueden dirigir al documento *"INN for pharmaceutical substances: Names for radicals, groups and others"**.

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SYAMNWVRQA PGKGLEWVST  50
TSGSGASTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKIW 100
IAFDIWGQGT MVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKRVEPKSCD KTHTCPPCPA PELLGGPSVF LFPPKPKDTL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPG      445
```

Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
GASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYGSSPYTFG 100
QGTKLEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                      215
```

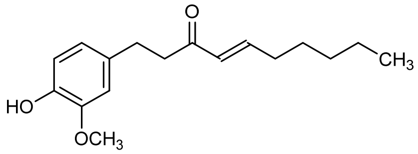
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 260-320 366-424
22''-96'' 143''-199'' 260''-320'' 366''-424''
Intra-L (C23-C104) 23'-89' 135'-195'
23'''-89''' 135'''-195'''
Inter-H-L (h 5-CL 126) * 219-215' 219''-215'''
Inter-H-H (h 11, h14) * 225-225'' 228-228''
*Two or three of the inter-chain disulfide bridges are not present, an average of 4 cysteinyl being conjugated each via a thioether bond to a drug linker.
*Deux ou trois des ponts disulfures inter-chaînes ne sont pas présents, 4 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.
*Faltan dos o tres puentes disulfuro inter-catenarios, una media de 4 cisteinil está conjugada a conectores de principio activo.

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
296, 296''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

enexasogaolum

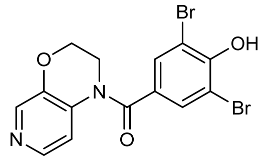
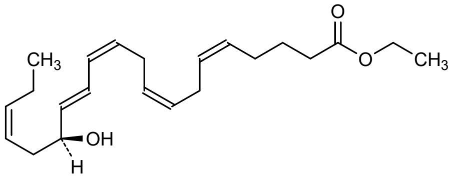
enexasogaol	(4*E*)-1-(4-hydroxy-3-methoxyphenyl)dec-4-en-3-one
énexasogaol	(4*E*)-1-(4-hydroxy-3-méthoxyphényl)déc-4-én-3-one
enexasogaol	(4*E*)-1-(4-hidroxi-3-metoxifenil)dec-4-en-3-ona

$C_{17}H_{24}O_3$

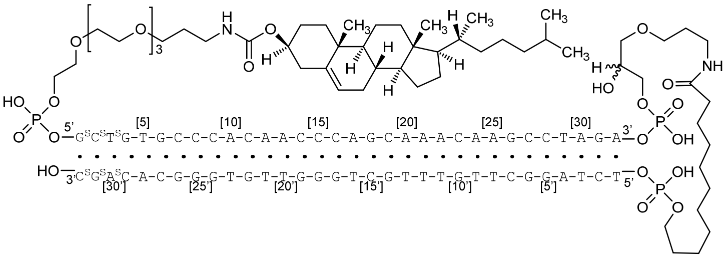


epaminuradum

epaminurad	(3,5-dibromo-4-hydroxyphenyl)(2,3-dihydro-4*H*-pyrido[4,3-*b*]-1,4-oxazin-4-yl)methanone
épaminurad	(3,5-dibromo-4-hydroxyphényl)(2,3-dihydro-4*H*-pyrido[4,3-*b*]-1,4-oxazin-4-yl)méthanone
epaminurad	(3,5-dibromo-4-hidroxifenil)(2,3-dihidro-4*H*-pirido[4,3-*b*]-1,4-oxazin-4-il)metanona

	$C_{14}H_{10}Br_2N_2O_3$
	
epeleutonum	
epeleuton	ethyl (5*Z*,8*Z*,11*Z*,13*E*,15*S*,17*Z*)-15-hydroxyicosa-5,8,11,13,17-pentaenoate
épéleuton	(5*Z*,8*Z*,11*Z*,13*E*,15*S*,17*Z*)-15-hydroxyicosa-5,8,11,13,17-pentaénoate d'éthyle
epeleutón	(5*Z*,8*Z*,11*Z*,13*E*,15*S*,17*Z*)-15-hidroxiicosa-5,8,11,13,17-pentaenoato de etilo
	$C_{22}H_{34}O_3$
	
etidaligidum	
etidaligide	*all-P-ambo*-5'-*O*-{(4*RS*)-1-[5'-*O*-{19-[(cholest-5-en-3β-yl)oxy]-1-hydroxy-1,19-dioxo-2,5,8,11,14-pentaoxa-18-aza-$1\lambda^{5}$-phosphanonadecan-1-yl}deoxy([1,2,3]tri-*P*-thio)(5'-GCTGTGCCCA CAACCCAGCA AACAAGCCTA GA-3')-3'-*O*-yl]-1,4,23-trihydroxy-1,11,23-trioxo-2,6,22-trioxa-10-aza-$1\lambda^{5}$,$23\lambda^{5}$-diphosphatricosan-23-yl}deoxy([29,30,31]tri-*P*-thio)(5'-TCTAGGCTTG TTTGCTGGGT TGTGGGCACA GC-3')
étidaligide	*tout-P-ambo*-5'-*O*-{(4*RS*)-1-[5'-*O*-{19-[(cholest-5-en-3β-yl)oxy]-1-hydroxy-1,19-dioxo-2,5,8,11,14-pentaoxa-18-aza-$1\lambda^{5}$-phosphanonadécan-1-yl}désoxy([1,2,3]tri-*P*-thio)(5'-GCTGTGCCCA CAACCCAGCA AACAAGCCTA GA-3')-3'-*O*-yl]-1,4,23-trihydroxy-1,11,23-trioxo-2,6,22-trioxa-10-aza-$1\lambda^{5}$,$23\lambda^{5}$-diphosphatricosan-23-yl}désoxy([29,30,31]tri-*P*-thio)(5'-TCTAGGCTTG TTTGCTGGGT TGTGGGCACA GC-3')
etidaligida	*todo-P-ambo*-5'-*O*-{(4*RS*)-1-[5'-*O*-{19-[(cholest-5-en-3β-yl)oxi]-1-hidroxi-1,19-dioxo-2,5,8,11,14-pentaoxa-18-aza-$1\lambda^{5}$-fosfanonadecan-1-yl}desoxi([1,2,3]tri-*P*-tio)(5'-GCTGTGCCCA CAACCCAGCA AACAAGCCTA GA-3')-3'-*O*-yl]-1,4,23-trihidroxi-1,11,23-trioxo-2,6,22-trioxa-10-aza-$1\lambda^{5}$,$23\lambda^{5}$-difosfatricosan-23-il}desoxi([29,30,31]tri-*P*-tio)(5'-TCTAGGCTTG TTTGCTGGGT TGTGGGCACA GC-3')

$C_{678}H_{885}N_{244}O_{392}P_{65}S_{6}$



etigilimabum #

etigilimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* TIGIT (T-cell immunoreceptor with Ig domain and ITIM, V-set Ig member 9, VSIG9, V-set and transmembrane member 3, VSTM3)], humanized monoclonal antibody;
gamma1 heavy chain (1-448) [*Homo sapiens* VH (IGHV4-59*01 (88.8%) -(IGHD)- IGHJ4*01 (92.9%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), hinge (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-33*01 (85.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*05, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (227-227'':230-230'')-bisdisulfide

étigilimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* TIGIT (immunorécepteur des lymphocytes T avec domaine Ig et ITIM, membre 9 de l'Ig V-set, VSIG9, membre 3 de l'Ig V-set et région transmembrane, VSTM3)], anticorps monoclonal humanisé;
chaîne lourde gamma1 (1-448) [*Homo sapiens* VH (IGHV4-59*01 (88.8%) -(IGHD)- IGHJ4*01 (92.9%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), charnière (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-33*01 (85.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*05, Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (227-227'':230-230'')-bisdisulfure

etigilimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TIGIT (inmunoreceptor de los linfocitos T con dominio Ig e ITIM, miembro 9 de la Ig V-set, VSIG9, miembro 3 de la Ig V-set y región transmembrana, VSTM3)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 (1-448) [*Homo sapiens* VH (IGHV4-59*01 (88.8%) -(IGHD)- IGHJ4*01 (92.9%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), bisagra (217-231), CH2 (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-33*01 (85.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*05, Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (227-227'':230-230'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada
QVQLQESGPG LVKPSETLSL TCAVSGYSIT SDYAWNWIRQ PPGKGLEWIG 50
YISYSGSTSY NPSLRSRVTI SRDTSKNQFF LKLSSVTAAD TAVYYCARRQ 100
VGLGFAYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK 448

Light chain / Chaîne légère / Cadena ligera
DIQMTQSPSS LSASVGDRVT ITCKASQDVS TAVAWYQQKP GKAPKLLIYS 50
ASYRYTGVPS RFSGSGSGTD FTFTISSLQP EDIATYYCQQ HYSTPWTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSNTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC 214

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22''-96'' 145''-201'' 262''-322'' 368''-426''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 221-214' 221''-214'''
Inter-H-H (h 11, h 14) 227-227'' 230-230''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
298, 298''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

faricimabum #

faricimab

immunoglobulin G1-kappa/lambda with domain crossover, anti-[*Homo sapiens* VEGFA (vascular endothelial growth factor A, VEGF-A, VEGF)] and anti-[*Homo sapiens* ANGPT2 (angiopoietin 2, Ang2)], humanized and *Homo sapiens* monoclonal antibody, bispecific; gamma1 heavy chain anti-VEGFA (1-453) [humanized VH (*Homo sapiens* IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), hinge 1-15 (222-236), CH2 [L1.3>A (240), L1.2>A (241), I15.2>A (259), H93>A (316), P114>G (335)](237-346), CH3D12 (362), L14 (364) [S10>C (360), T22>W (372), H115>A (441)](347-451), CHS (452-453)) (124-453)], (226-214')-disulfide with kappa light chain, anti-VEGFA (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-16*01 (87.4%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; gamma1-kappa heavy chain anti-ANGPT2 (1''-463'') [*Homo sapiens* VH (IGHV1-2*02 (100%)-(IGHD)-IGHJ3*02 (100%)) [8.8.22] (1''-129'') -*Homo sapiens* IGKC*01, Km3 A45.1 (175), V101 (213) [R1.4>A (130), T1.3>S (131)] (130''-236'') -*Homo sapiens* IGHG1*01, G1m1 (hinge 6-15 (237-246), (CH2[L1.3>A (250), L1.2>A (251), I15.2>A (269), H93>A (326), P114>G (345)] (247-356), CH3 D12 (372), L14 (374) [Y5>C (365),T22>S (382), L24>A (384), Y86>V (423), H115>A (451)] (357-461), CHS (462-463)) (237''-463'')], (236''-213''')-disulfide with lambda-gamma light chain anti-ANGPT2 (1'''-213''') [*Homo sapiens* V-LAMBDA (IGLV3-21*02 (100.00%) -IGLJ2*01 (100%)) [6.3.11] (1'''-108''') -2-mer linker biseryl (109'''-110''') -*Homo sapiens* IGHG1*01, G1m17(CH1 K120 (207) (111-208)-hinge 1-5 (209-213)) (111'''-213''')]; dimer (232-242'':235-245'':360-365'')-trisdisulfide

faricimab

immunoglobuline G1-kappa/lambda avec domaines échangés, anti-[*Homo sapiens* VEGFA (facteur de croissance A de l'endothélium vasculaire, VEGF-A, VEGF)] et anti-[*Homo sapiens* ANGPT2 (angiopoiétine 2, Ang2)], anticorps monoclonal humanisé et *Homo sapiens*, bispécifique;

chaîne lourde gamma1 anti-VEGFA (1-453) [VH humanisé (*Homo sapiens* IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), charnière 1-15 (222-236), CH2 [L1.3>A (240), L1.2>A (241), I15.2>A (259), H93>A (316), P114>G (335)](237-346), CH3D12 (362), L14 (364) [S10>C (360), T22>W (372), H115>A (441)](347-451), CHS (452-453)) (124-453)], (226-214')-disulfure avec la chaîne légère kappa, anti-VEGFA (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-16*01 (87.4%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')];
chaîne lourde gamma1-kappa anti-ANGPT2 (1''-463'') [*Homo sapiens* VH (IGHV1-2*02 (100%) -(IGHD)-IGHJ3*02 (100%)) [8.8.22] (1''-129'') -*Homo sapiens* IGKC*01, Km3 A45.1 (175), V101 (213) [R1.4>A (130), T1.3>S (131)] (130''-236'') -*Homo sapiens* IGHG1*01, G1m1 (charnière 6-15 (237-246), (CH2 [L1.3>A (250), L1.2>A (251), I15.2>A (269), H93>A (326), P114>G (345)] (247-356), CH3 D12 (372), L14 (374) [Y5>C (365), T22>S (382), L24>A (384), Y86>V (423), H115>A (451)] (357-461), CHS (462-463)) (237''-463'')], (236''-213''')-disulfure avec la chaîne légère lambda-gamma anti-ANGPT2 (1'''-213''') [*Homo sapiens* V-LAMBDA (IGLV3-21*02 (100.00%) -IGLJ2*01 (100%)) [6.3.11] (1'''-108''') -2-mer linker biséryl (109'''-110''') -*Homo sapiens* IGHG1*01,G1m17 (CH1 K120 (207) (111-208)-charnière 1-5 (209-213)) (111'''-213''')]; dimère (232-242'':235-245'':360-365'')-trisdisulfure

faricimab

inmunoglobulina G1-kappa/lambda con dominios intercambiados,anti-[*Homo sapiens* VEGFA (factor de crecimiento A del endotelio vascular, VEGF-A, VEGF)] y anti-[*Homo sapiens* ANGPT2 (angiopoyetina 2, Ang2)], anticuerpo monoclonal humanizado y *Homo sapiens*, biespecífico;
cadena pesada gamma1 anti-VEGFA (1-453) [VH humanizado (*Homo sapiens* IGHV3-30*02 (75.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.16] (1-123) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (220) (124-221), bisagra 1-15 (222-236), CH2 [L1.3>A (240), L1.2>A (241), I15.2>A (259), H93>A (316), P114>G (335)](237-346), CH3D12 (362), L14 (364) [S10>C (360), T22>W (372), H115>A (441)](347-451), CHS (452-453)) (124-453)], (226-214')-disulfuro con la cadena ligera kappa,anti-VEGFA (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-16*01 (87.4%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')];
cadena pesada gamma1-kappa anti-ANGPT2 (1''-463'') [*Homo sapiens* VH (IGHV1-2*02 (100%) -(IGHD)-IGHJ3*02 (100%)) [8.8.22] (1''-129'') -*Homo sapiens* IGKC*01, Km3 A45.1 (175), V101 (213) [R1.4>A (130), T1.3>S (131)] (130''-236'') -*Homo sapiens* IGHG1*01, G1m1 (bisagra 6-15 (237-246), (CH2 [L1.3>A (250), L1.2>A (251), I15.2>A (269), H93>A (326), P114>G (345)] (247-356), CH3 D12 (372), L14 (374) [Y5>C (365), T22>S (382), L24>A (384), Y86>V (423), H115>A (451)] (357-461), CHS (462-463)) (237''-463'')], (236''-213''')-disulfuro con la cadena ligera lambda-gamma anti-ANGPT2 (1'''-213''') [*Homo sapiens* V-LAMBDA (IGLV3-21*02 (100.00%) -IGLJ2*01 (100%)) [6.3.11] (1'''-108''') -2-mer ligando biseril (109'''-110''') -*Homo sapiens* IGHG1*01,G1m17 (CH1 K120 (207) (111-208)-bisagra 1-5 (209-213)) (111'''-213''')]; dímero (232-242'':235-245'':360-365'')-trisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada anti-VEGFA

```
EVQLVESGGG LVQPGGSLRL SCAASGYDFT HYGMNWVRQA PGKGLEWVGW  50
INTYTGEPTY AADFKRRFTF SLDTSKSTAY LQMNSLRAED TAVYYCAKYP 100
YYYGTSHWYF DVWGQGTLVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC 150
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG 200
TQTYICNVNH KPSNTKVDKK VEPKSCDKTH TCPPCPAPEA AGGPSVFLFP 250
PKPKDTLMAS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE 300
QYNSTYRVVS VLTVLAQDWL NGKEYKCKVS NKALGAPIEK TISKAKGQPR 350
EPQVYTLPPC RDELTKNQVS LWCLVKGFYP SDIAVEWESN GQPENNYKTT 400
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN AYTQKSLSLS 450
PGK                                                   453
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Light chain / Chaîne légère / Cadena ligera anti-VEGFA

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DIQLTQSPSS LSASVGDRVT ITCSASQDIS NYLNWYQQKP GKAPKVLIYF  50
TSSLHSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ YSTVPWTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                       214
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Heavy chain / Chaîne lourde / Cadena pesada anti-ANGPT2

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT GYYMHWVRQA PGQGLEWMGW  50
INPNSGGTNY AQKFQGRVTM TRDTSISTAY MELSRLRSDD TAVYYCARSP 100
NPYYYDSSGY YYPGAFDIWG QGTMVTVSSA SVAAPSVFIF PPSDEQLKSG 150
TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST 200
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGECDKTH TCPPCPAPEA 250
AGGPSVFLFP PKPKDTLMAS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV 300
HNAKTKPREE QYNSTYRVVS VLTVLAQDWL NGKEYKCKVS NKALGAPIEK 350
TISKAKGQPR EPQVCTLPPS RDELTKNQVS LSCAVKGFYP SDIAVEWESN 400
GQPENNYKTT PPVLDSDGSF FLVSKLTVDK SRWQQGNVFS CSVMHEALHN 450
AYTQKSLSLS PGK                                        463
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Light chain / Chaîne légère / Cadena ligera anti-ANGPT2

```
SYVLTQPPSV SVAPGQTARI TCGGNNIGSK SVHWYQQKPG QAPVLVVYDD  50
SDRPSGIPER FSGSNSGNTA TLTISRVEAG DEADYYCQVW DSSSDHWVFG 100
GGTKLTVLSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS 150
WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS 200
NTKVDKKVEP KSC                                        213
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 150-206 267-327 373-431
22"-96" 156"-216" 277"-337" 383"-441"
Intra-L (C23-C104) 23'-88' 134'-194'
22'''-87''' 137'''-193'''
Inter-H-L (h 5-CL 126) 226-214' 236"-213'''
Inter-H-H (h 11, h 14, AA >C) 232-242" 235-245" 360-365"
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4 :
303, 313"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

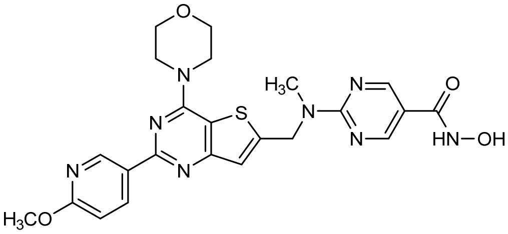
fidanacogenum elaparvovecum #

fidanacogene elaparvovec	a non-replicating adeno-associated virus serotype 2 (AAV2) expressing the Padua variant (R338L) of human coagulation factor IX (F9, Factor IX, FIX), under the control of the liver-specific apolipoprotein E (Apo E) enhancer/alpha1-antitrypsin (hAAT) promoter (ApoE/hAAT), and all AAV genes encoding viral products deleted
fidanacogène élaparvovec	virus adéno-associé de sérotype 2 (AAV2) non-répliquant, exprimant le variant Padua (R338L) du facteur de coagulation IX humain (F9, Facteur IX, FIX), sous le contrôle de l'activateur de l'apolipoprotéine E (ApoE) spécifique du foie/promoteur de l'alpha1-antitrypsine (ApoE/hAAT) et tous les gènes de l'AAV codant pour des produits viraux ont été supprimés
fidanacogén elaparvovec	un virus adenoasociado de serotipo 2 (AAV2) no replicativo, que expresa la variante Padua (R338L) del factor de coagulación IX (F9, también conocido como Factor IX (FIX)), bajo el control del enhancer de la apolipoproteína E (Apo E) específica del hígado/promotor de la alfa1-antitripsina (hAAT) (ApoE/hAAT), y con todos los genes del AAV que codifican para productos del virus delecionados

fimepinostatum

fimepinostat	*N*-hydroxy-2-[{[2-(6-methoxypyridin-3-yl)-4-(morpholin-4-yl)thieno[3,2-*d*]pyrimidin-6-yl]methyl}(methyl)amino]pyrimidine-5-carboxamide
fimépinostat	*N*-hydroxy-2-[{[2-(6-méthoxypyridin-3-yl)-4-(morpholin-4-yl)thiéno[3,2-*d*]pyrimidin-6-yl]méthyl}(méthyl)amino]pyrimidine-5-carboxamide
fimepinostat	*N*-hidroxi-2-[{[2-(6-metoxipiridin-3-il)-4-(morfolin-4-il)tieno[3,2-*d*]pirimidin-6-il]metil}(metil)amino]pirimidina-5-carboxamida

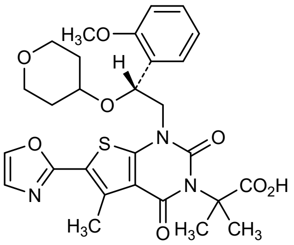
$C_{23}H_{24}N_8O_4S$



firsocostatum

firsocostat	2-[1-{(2*R*)-2-(2-methoxyphenyl)-2-[(oxan-4-yl)oxy]ethyl}-5-methyl-6-(1,3-oxazol-2-yl)-2,4-dioxo-1,4-dihydrothieno[2,3-*d*]pyrimidin-3(2*H*)-yl]-2-methylpropanoic acid
firsocostat	acide 2-[1-{(2*R*)-2-(2-méthoxyphényl)-2-[(oxan-4-yl)oxy]éthyl}-5-méthyl-6-(1,3-oxazol-2-yl)-2,4-dioxo-1,4-dihydrothiéno[2,3-*d*]pyrimidin-3(2*H*)-yl]-2-méthylpropanoïque
firsocostat	ácido 2-[1-{(2*R*)-2-(2-metoxifenil)-2-[(oxan-4-il)oxi]etil}-5-metil-6-(1,3-oxazol-2-il)-2,4-dioxo-1,4-dihidrotieno[2,3-*d*]pirimidin-3(2*H*)-il]-2-metilpropanoico

$C_{28}H_{31}N_3O_8S$



flotetuzumabum #

flotetuzumab	immunoglobulin scFv_scFv, anti-[*Homo sapiens* IL3RA (interleukin 3 receptor subunit alpha, interleukin 3 receptor alpha (low affinity), CD123)] and anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)]; *Mus musculus* and humanized monoclonal antibody scFv_scFv, bispecific;

	scFv-lambda-heavy-E-coil (1-272) [V-LAMBDA anti-CD3E (*Mus musculus* IGLV1-01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46 (77.9%) -IGHJ3*02 (100%)) [9.3.9] (1-109) -9-mer tetraglycyl-seryl-tetraglycyl linker (110-118) -humanized VH anti-IL3RA (*Homo sapiens* IGHV1-46*01 (83.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.13] (119-238)-6-mer diglycyl-cysteinyl-triglycyl linker (239-244) -E-coil motif (245-272)], (241-249')-disulfide with scFv-kappa-heavy-K-coil (1'-280') [V-KAPPA anti-IL3RA (*Mus musculus* IGKV8-19*01 (91.1%) -IGKJ2*01 (91.7%)/*Homo sapiens* IGKV4-1*01 (88.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -8-mer triglycyl-seryl-tetraglycyl linker (114'-121') -VH anti-CD3E (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (93.9%)/*Homo sapiens* IGHV3-72*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (122'-246')] -6-mer diglycyl-cysteinyl-triglycyl linker (247'-252') -K-coil motif (253'-280')]
flotétuzumab	immunoglobuline scFv_scFv, anti-[*Homo sapiens* IL3RA (sous-unité alpha du récepteur de l'interleukine 3, récepteur alpha (faible affinité) de l'interleukine 3, CD123)] et anti-[*Homo sapiens* CD3E (CD3 epsilon, Leu-4)]; anticorps monoclonal scFv_scFv *Mus musculus* et humanisé, bispécifique; scFv-lambda-lourde-E-coil (1-272) [V-LAMBDA anti-CD3E (*Mus musculus* IGLV1-01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46 (77.9%) -IGHJ3*02 (100%)) [9.3.9] (1-109) -9-mer tétraglycyl-séryl-tétraglycyl linker (110-118) -VH anti-IL3RA humanisé (*Homo sapiens* IGHV1-46*01 (83.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.13] (119-238)-6-mer diglycyl-cystéinyl-triglycyl linker (239-243) -motif E-coil (245-272)], (241-249')-disulfure avec scFv-kappa-lourde-K-coil (1'-280') [V-KAPPA anti-IL3RA (*Mus musculus* IGKV8-19*01 (91.1%) -IGKJ2*01 (91.7%)/*Homo sapiens* IGKV4-1*01 (88.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -8-mer triglycyl-séryl-tétraglycyl linker (114'-121') -VH anti-CD3E (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (93.9%)/*Homo sapiens* IGHV3-72*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (122'-246')] -6-mer diglycyl-cystéinyl-triglycyl linker (247'-252')-motif K-coil (253'-280')]
flotetuzumab	inmunoglobulina scFv_scFv, anti-[*Homo sapiens* IL3RA (subunidad alfa del receptor de la interleukina 3, receptor alfa (baja afinidad) de la interleukina 3, CD123)]yt anti-[*Homo sapiens* CD3E (CD3 épsilon, Leu-4)]; *Mus musculus* y anticuerpo monoclonal humanizado scFv_scFv, biespecífico; scFv-lambda-pesada-E-coil (1-272) [V-LAMBDA anti-CD3E (*Mus musculus* IGLV1-01 (81.2%) -IGLJ1*01 (100%)/*Homo sapiens* IGLV7-46 (77.9%) -IGHJ3*02 (100%)) [9.3.9] (1-109) -9-mer tetraglicil-seril-tetraglicil ligando (110-118) -VH anti-IL3RA humanizado (*Homo sapiens* IGHV1-46*01 (83.7%) -(IGHD) -IGHJ6*01 (90.9%)) [8.8.13] (119-238)-6-mer diglicil-cisteinil-triglicil ligando (239-243) -motif E-coil (245-272)], (241-249')-disulfuro con scFv-kappa-pesada-K-coil (1'-280') [V-KAPPA anti-IL3RA (*Mus musculus* IGKV8-19*01 (91.1%) -IGKJ2*01 (91.7%)/*Homo sapiens* IGKV4-1*01 (88.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -8-mer triglicil-seril-tetraglicil ligando (114'-121') -VH anti-CD3E (*Mus musculus* IGHV10-1*02 (89.9%) -(IGHD) -IGHJ3*01 (93.9%)/*Homo sapiens* IGHV3-72*01 (87.0%) -(IGHD) -IGHJ6*01 (90.9%)) [8.10.16] (122'-246')] -6-mer diglicil-cisteinil-triglicil ligando (247'-252') -motif K-coil (253'-280')]

scFv-lambda-heavy-E-coil

```
QAVVTQEPSL TVSPGGTVTL TCRSSTGAVT TSNYANWVQQ KPGQAPRGLI  50
GGTNKRAPWT PARFSGSLLG GKAALTITGA QAEDEADYYC ALWYSNLWVF 100
GGGTKLTVLG GGGSGGGGEV QLVQSGAELK KPGASVKVSC KASGYTFTDY 150
YMKWVRQAPG QGLEWIGDII PSNGATFYNQ KFKGRVTITV DKSTSTAYME 200
LSSLRSEDTA VYYCARSHLL RASWFAYWGQ GTLVTVSSGG CGGGEVAALE 250
KEVAALEKEV AALEKEVAAL EK                               272
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scFv-kappa-heavy-K-coil

```
DFVMTQSPDS LAVSLGERVT MSCKSSQSLL NSGNQKNYLT WYQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNDYSY 100
PYTFGQGTKL EIKGGGSGGG GEVQLVESGG GLVQPGGSLR LSCAASGFTF 150
STYAMNWVRQ APGKGLEWVG RIRSKYNNYA TYYADSVKDR FTISRDDSKN 200
SLYLQMNSLK TEDTAVYYCV RHGNFGNSYV SWFAYWGQGT LVTVSSGGCG 250
GGKVAALKEK VAALKEKVAA LKEKVAALKE                       280
```

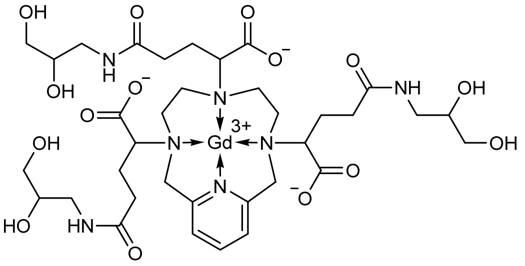
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-scFv (C23-C104) 22-90 140-214
23'-94' 143'-219'
Inter-chain (h 11, h 14) 241-249'

No N-glycosylation sites / pas de sites de N-glycosylation / ningún position de N-glicosilación
N-terminal glutamine cyclization to Glp (5-oxoproline, pyroglutamic acid):
Q1>Glp (1)

gadopiclenolum

gadopiclenol	*rac*-[(2*R*,2'*Ξ*,2''*Ξ*)-2,2',2''-(3,6,9-triaza-κ^{3}*N*^{3},*N*^{6},*N*^{9}-1(2,6)-pyridina-κ*N*^{1}-cyclodecaphane-3,6,9-triyl)tris(5-{[(2*Ξ*)-2,3-dihydroxypropyl]amino}-5-oxopentanoato-κ^{3}*O*^{1},*O*$^{1'}$,*O*$^{1''}$)(3−)]gadolinium
gadopiclénol	*rac*-[(2*R*,2'*Ξ*,2''*Ξ*)-2,2',2''-(3,6,9-triaza-κ^{3}*N*^{3},*N*^{6},*N*^{9}-1(2,6)-pyridina-κ*N*^{1}-cyclodécaphane-3,6,9-triyl)tris(5-{[(2*Ξ*)-2,3-dihydroxypropyl]amino}-5-oxopentanoato-κ^{3}*O*^{1},*O*$^{1'}$,*O*$^{1''}$)(3−)]gadolinium
gadopiclenol	*rac*-[(2*R*,2'*Ξ*,2''*Ξ*)-2,2',2''-(3,6,9-triaza-κ^{3}*N*^{3},*N*^{6},*N*^{9}-1(2,6)-piridina-κ*N*^{1}-ciclodecafano-3,6,9-triil)tris(5-{[(2*Ξ*)-2,3-dihidroxipropil]amino}-5-oxopentanoato-κ^{3}*O*^{1},*O*$^{1'}$,*O*$^{1''}$)(3−)]gadolinio

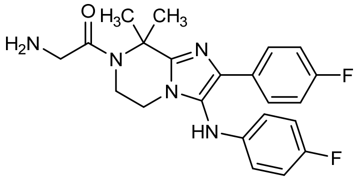
$C_{35}H_{54}GdN_{7}O_{15}$



ganaplacidum

ganaplacide	2-amino-1-[3-(4-fluoroanilino)-2-(4-fluorophenyl)-8,8-dimethyl-5,6-dihydroimidazo[1,2-*a*]pyrazin-7(8*H*)-yl]ethan-1-one
ganaplacide	2-amino-1-[3-(4-fluoroanilino)-2-(4-fluorophényl)-8,8-diméthyl-5,6-dihydroimidazo[1,2-*a*]pyrazin-7(8*H*)-yl]éthan-1-one
ganaplacida	2-amino-1-[3-(4-fluoroanilino)-2-(4-fluorofenil)-8,8-dimetil-5,6-dihidroimidazo[1,2-*a*]pirazin-7(8*H*)-il]etan-1-ona

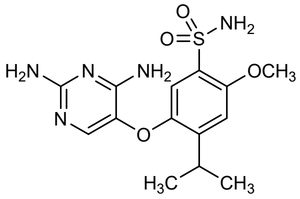
$C_{22}H_{23}F_2N_5O$



gefapixantum

gefapixant	5-[(2,4-diaminopyrimidin-5-yl)oxy]-2-methoxy-4-(propan-2-yl)benzene-1-sulfonamide
géfapixant	5-[(2,4-diaminopyrimidin-5-yl)oxy]-2-méthoxy-4-(propan-2-yl)benzène-1-sulfonamide
gefapixant	5-[(2,4-diaminopirimidin-5-il)oxi]-2-metoxi-4-(propan-2-il)benceno-1-sulfonamida

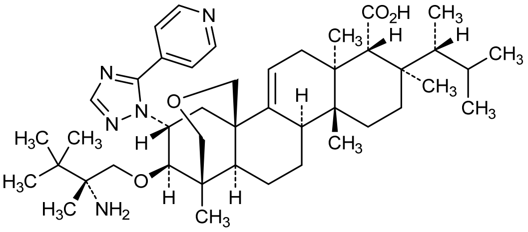
$C_{14}H_{19}N_5O_4S$



ibrexafungerpum

ibrexafungerp	(1*S*,4a*R*,6a*S*,7*R*,8*R*,10a*R*,10b*R*,12a*R*,14*R*,15*R*)-15-[(2*R*)-2-amino-2,3,3-trimethylbutoxy]-1,6a,8,10a-tetrameth-yl-8-[(2*R*)-3-methylbutan-2-yl]-14-[5-(pyridin-4-yl)-1*H*-1,2,4-triazol-1-yl]-1,6,6a,7,8,9,10,10a,10b,11,12,12a-dodecahydro-2*H*,4*H*-1,4a-propanophenanthro[1,2-*c*]pyran-7-carboxylic acid
ibrexafungerp	acide (1*S*,4a*R*,6a*S*,7*R*,8*R*,10a*R*,10b*R*,12a*R*,14*R*,15*R*)-15-[(2*R*)-2-amino-2,3,3-triméthylbutoxy]-1,6a,8,10a-tétraméth-yl-8-[(2*R*)-3-méthylbutan-2-yl]-14-[5-(pyridin-4-yl)-1*H*-1,2,4-triazol-1-yl]-1,6,6a,7,8,9,10,10a,10b,11,12,12a-dodécahydro-2*H*,4*H*-1,4a-propanophénanthro[1,2-*c*]pyran-7-carboxylique
ibrexafungerp	ácido (1*S*,4a*R*,6a*S*,7*R*,8*R*,10a*R*,10b*R*,12a*R*,14*R*,15*R*)-15-[(2*R*)-2-amino-2,3,3-trimetilbutoxi]-1,6a,8,10a-tetramet-il-8-[(2*R*)-3-metilbutan-2-il]-14-[5-(piridin-4-il)-1*H*-1,2,4-triazol-1-il]-1,6,6a,7,8,9,10,10a,10b,11,12,12a-dodecahidro-2*H*,4*H*-1,4a-propanofenantro[1,2-*c*]piran-7-carboxílico

$C_{44}H_{67}N_5O_4$



imaprelimabum #
imaprelimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* MCAM (melanoma cell adhesion molecule, gicerin, MUC18, CD146)], humanized monoclonal antibody;
gamma1 heavy chain (1-448) [humanized VH (*Homo sapiens* IGHV2-26*01 (82.0%) -(IGHD)-IGHJ4*01 (93.3%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), hinge (217-231), CH2 L1.3>A (235), L1.2>A (236) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-213')-disulfide with kappa light chain (1'-213') [humanized V-KAPPA (*Homo sapiens* IGKV1-12*01 (85.6%) -IGKJ2*01 (100%)) [6.3.8] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (152), V101 (190) (107'-213')]; dimer (227-227'':230-230'')-bisdisulfide

imaprélimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* MCAM (molécule d'adhésion de cellule de mélanome, gicérine, MUC18, CD146)], anticorps monoclonal humanisé;
chaîne lourde gamma1 (1-448) [VH humanisé (*Homo sapiens* IGHV2-26*01 (82.0%) -(IGHD)-IGHJ4*01 (93.3%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), charnière (217-231), CH2 L1.3>A (235), L1.2>A (236)(232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-213')-disulfure avec la chaîne légère kappa (1'-213') [V-KAPPA humanisé (*Homo sapiens* IGKV1-12*01 (85.6%) -IGKJ2*01 (100%)) [6.3.8] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (152), V101 (190) (107'-213')]; dimère (227-227'':230-230'')-bisdisulfure

imaprelimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* MCAM (molécula de adhesión de célula de melanoma, gicerina, MUC18, CD146)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 (1-448) [VH humanizado (*Homo sapiens* IGHV2-26*01 (82.0%) -(IGHD)-IGHJ4*01 (93.3%)) [8.7.12] (1-118) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (215) (119-216), bisagra (217-231), CH2 L1.3>A (235), L1.2>A (236) (232-341), CH3 E12 (357), M14 (359) (342-446), CHS (447-448)) (119-448)], (221-213')-disulfuro con la cadena ligera kappa (1'-213') [V-KAPPA humanizado (*Homo sapiens* IGKV1-12*01 (85.6%) -IGKJ2*01 (100%)) [6.3.8] (1'-106') -*Homo sapiens* IGKC*01, Km3 A45.1 (152), V101 (190) (107'-213')]; dímero (227-227'':230-230'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVTLKESGPV LVKPTETLTL TCTVSGFSLT SNAVSWVRQP PGKALEWIAA  50
ISSGGTTYYN SAFKSRLTIS RDTSKSQVVL TMTNMDPVDT ATYYCARRYG 100
YGWYFDFWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPEAAGGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TLPPSREEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK   448
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT INCKASQNIY NSLAWYQQKP GKAPKVLIFN  50
ANSLQTGIPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ FYSGYTFGQG 100
TKLEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD 150
NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL 200
SSPVTKSFNR GEC                                         213
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-95 145-201 262-322 368-426
22''-95'' 145''-201'' 262''-322'' 368''-426''
Intra-L (C23-C104) 23'-88' 133'-193'
23'''-88''' 133'''-193'''
Inter-H-L (h 5-CL 126) 221-213' 221''-213'''
Inter-H-H (h 11, h 14) 227-227'' 230-230''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
298, 298''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

iscalimabum #

iscalimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD40 (tumor necrosis factor receptor superfamily member 5, TNFRSF5)], human monoclonal antibody;
gamma1 heavy chain (1-450) [*Homo sapiens* VH (IGHV3-30*03 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03, G1m3, nG1m1 (CH1 R120 (217) (121-218), hinge (219-233), CH2 N84.4>A (300) (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-219')-disulfide with kappa light chain (1'-219') [*Homo sapiens* V-KAPPA (IGKV2-28*01 (95.0%) -IGKJ3*01 (91.7%, K12>R)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (229-229'':232-232'')-bisdisulfide

iscalimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD40 (membre 5 de la superfamille des récepteurs du TNF, TNFRSF5)], anticorps monoclonal humain;
chaîne lourde gamma1 (1-450) [*Homo sapiens* VH (IGHV3-30*03 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03 (CH1 (121-218), charnière (219-233), CH2 N84.4>A (300) (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-219')-disulfure avec la chaîne légère kappa (1'-219') [*Homo sapiens* V-KAPPA (IGKV2-28*01 (95.0%) -IGKJ3*01 (91.7%, K12>R) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (229-229'':232-232'')-bisdisulfure

iscalimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD40 (miembro 5 de la superfamilia de los receptores del TNF, TNFRSF5)], anticuerpo monoclonal humano;
cadena pesada gamma1 (1-450) [*Homo sapiens* VH (IGHV3-30*03 (93.9%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03 (CH1 (121-218), bisagra (219-233), CH2 N84.4>A (300) (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-219')-disulfuro con la cadena ligera kappa (1'-219') [*Homo sapiens* V-KAPPA (IGKV2-28*01 (95.0%) -IGKJ3*01 (91.7%, K12>R) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (229-229'':232-232'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYGMHWVRQA PGKGLEWVAV  50
ISYEESNRYH ADSVKGRFTI SRDNSKITLY LQMNSLRTED TAVYYCARDG 100
GIAAPGPDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKRVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYA 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPLS LTVTPGEPAS ISCRSSQSLL YSNGYNYLDW YLQKPGQSPQ  50
VLISLGSNRA SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCMQARQTP 100
FTFGPGTKVD IRRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22''-96'' 147''-203'' 264''-324'' 370''-428''
Intra-L (C23-C104) 23'-93' 139'-199'
23'''-93''' 139'''-199'''
Inter-H-L (h 5-CL 126) 223-219' 223''-219'''
Inter-H-H (h 11, h 14) 229-229'' 232-232''

No N-glycosylation sites / pas de sites de N-glycosylation / ningún positión de N-glicosilación:
H CH2 N84.4>A (300, 300'')

N-terminal glutamine cyclization to Glp (5-oxoproline, pyroglutamic acid):
H VH Q1>Glp (1, 1'')

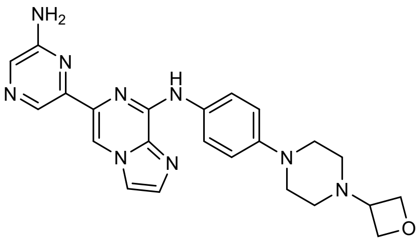
C-terminal lysine clipping:
H CHS K2: 450, 450''

lanraplenibum
lanraplenib 6-(6-aminopyrazin-2-yl)-*N*-{4-[4-(oxetan-3-yl)piperazin-1-yl]phenyl}imidazo[1,2-*a*]pyrazin-8-amine

lanraplénib 6-(6-aminopyrazin-2-yl)-*N*-{4-[4-(oxétan-3-yl)pipérazin-1-yl]phényl}imidazo[1,2-*a*]pyrazin-8-amine

lanraplenib 6-(6-aminopirazin-2-il)-*N*-{4-[4-(oxetan-3-il)piperazin-1-il]fenil}imidazo[1,2-*a*]pirazin-8-amina

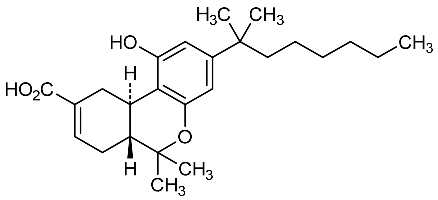
$C_{23}H_{25}N_9$



lenabasumum

lenabasum	(6a*R*,10a*R*)-1-hydroxy-6,6-dimethyl-3-(2-methyloctan-2-yl)-6a,7,10,10a-tetrahydro-6*H*-dibenzo[*b*,*d*]pyran-9-carboxylic acid
lénabasum	acide (6a*R*,10a*R*)-1-hydroxy-6,6-diméthyl-3-(2-méthyloctan-2-yl)-6a,7,10,10a-tétrahydro-6*H*-dibenzo[*b*,*d*]pyran-9-carboxylique
lenabasum	ácido (6a*R*,10a*R*)-1-hidroxi-6,6-dimetil-3-(2-metiloctan-2-il)-6a,7,10,10a-tetrahidro-6*H*-dibenzo[*b*,*d*]piran-9-carboxílico

$C_{25}H_{36}O_4$



lenvervimabum #

lenvervimab	immunoglobulin G1-kappa, anti-[Hepatitis B virus (HBV) surface antigen (HBsAg)], humanized monoclonal antibody; gamma1 heavy chain (1-459) [humanized VH (*Homo sapiens* IGHV3-21*01 (83.7%) -(IGHD) -IGHJ1*01 (90%), L12>T (124)) [8.8.22] (1-129) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (226) (130-227), hinge (228-242), CH2 (243-352), CH3 D12 (368), L14 (370) (353-457), CHS (458-459)) (130-459)], (232-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-NL1*01 (87.4%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (238-238'':241-241'')-bisdisulfide
lenvervimab	immunoglobuline G1-kappa, anti-[antigène de surface du virus de l'hépatite B (VHB) (AgsHB)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-459) [VH humanisé (*Homo sapiens* IGHV3-21*01 (83.7%) -(IGHD) -IGHJ1*01 (90%), L12>T (124)) [8.8.22] (1-129) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (226) (130-227), charnière (228-242), CH2 (243-352), CH3 D12 (368), L14 (370) (353-457), CHS (458-459)) (130-459)], (232-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-NL1*01 (87.4%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (238-238'':241-241'')-bisdisulfure

lenvervimab

inmunoglobulina G1-kappa, anti-[antígeno de superficie del virus de la hepatitis B (VHB) (AgsHB)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 (1-459) [VH humanizado (*Homo sapiens* IGHV3-21*01 (83.7%) -(IGHD) -IGHJ1*01 (90%), L12>T (124)) [8.8.22] (1-129) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (226) (130-227), bisagra (228-242), CH2 (243-352), CH3 D12 (368), L14 (370) (353-457), CHS (458-459)) (130-459)], (232-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-NL1*01 (87.4%) -IGKJ2*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (238-238'':241-241'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCSASGFSLT KYKMTWVRQA PGKGLEWVSS  50
ISSTSRDIDY ADSVKGRFTI SRDNAKNSLF LQMSSLRVDD TAVYYCTRDG 100
WLWGWDVRSN YYYNALDVWG QGTTVTVSSA STKGPSVFPL APSSKSTSGG 150
TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV 200
PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP 250
SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK 300
TKPREEQYNS TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK 350
AKGQPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE 400
NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ 450
KSLSLSPGK                                              459
```

Light chain / Chaîne légère / Cadena ligera

```
DIVVTQSPSS LSASVGDRVT ITCRASQGIY NSIAWYQQKP GKAPKLLLYS  50
TSTLLSGVPS RFSGSGSGTD YTLTITNLQP EDFATYYCQQ YFVTPETFGQ 100
GTKLEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 156-212 273-333 379-437
22''-96'' 156''-212'' 273''-333'' 379''-437''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 232-214' 232''-214'''
Inter-H-H (h 11, h 14) 238-238'' 241-241''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
309, 309''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

leronlimabum #

leronlimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* CCR5 (chemokine (C-C motif) receptor 5, CD195)], humanized monoclonal antibody;
gamma4 heavy chain (1-449) [humanized VH (*Homo sapiens* IGHV3-15*01 (72.40%) -(IGHD)-IGHJ4*01 (86.7%)) [7.8.16] (1-122) -*Homo sapiens* IGHG4*01 (CH1 (123-220), hinge (221-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-219')-disulfide with kappa light chain (1'-219') [humanized V-KAPPA (*Homo sapiens* IGKV2D-29*02 (87.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimer (228-228'':231-231'')-bisdisulfide

léronlimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* CCR5 (récepteur 5 de la chimiokine (motif C-C), CD195)], anticorps monoclonal humanisé;

chaîne lourde gamma4 (1-449) [VH humanisé (*Homo sapiens* IGHV3-15*01 (72.40%) -(IGHD)- IGHJ4*01 (86.7%)) [7.8.16] (1-122) -*Homo sapiens* IGHG4*01 (CH1 (123-220), charnière (221-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-219')-disulfure avec la chaîne légère kappa (1'-219') [V-KAPPA humanisé (*Homo sapiens* IGKV2D-29*02 (87.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dimère (228-228":231-231")-bisdisulfure

leronlimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* CCR5 (receptor 5 de la quimiocina (motif C-C), CD195)], anticuerpo monoclonal humanizado;
cadena pesada gamma4 (1-449) [VH humanizado (*Homo sapiens* IGHV3-15*01 (72.40%) -(IGHD)- IGHJ4*01 (86.7%)) [7.8.16] (1-122) -*Homo sapiens* IGHG4*01 (CH1 (123-220), bisagra (221-232), CH2 (233-342), CH3 (343-447), CHS (448-449)) (123-449)], (136-219')-disulfuro con la cadena ligera kappa (1'-219') [V-KAPPA humanizado (*Homo sapiens* IGKV2D-29*02 (87.0%) -IGKJ1*01 (100%)) [11.3.9] (1'-112') -*Homo sapiens* IGKC*01, Km3 A45.1 (158), V101 (196) (113'-219')]; dímero (228-228":231-231")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGYTFS NYWIGWVRQA PGKGLEWIGD  50
IYPGGNYIRN NEKFKDKTTL SADTSKNTAY LQMNSLKTED TAVYYCGSSF 100
GSNYVFAWFT YWGQGTLVTV SSASTKGPSV FPLAPCSRST SESTAALGCL 150
VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ SSGLYSLSSV VTVPSSSLGT 200
KTYTCNVDHK PSNTKVDKRV ESKYGPPCPS CPAPEFLGGP SVFLFPPKPK 250
DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV 350
YTLPPSQEEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL 400
DSDGSFFLYS RLTVDKSRWQ EGNVFSCSVM HEALHNHYTQ KSLSLSLGK  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPLS LPVTPGEPAS ISCRSSQRLL SSYGHTYLHW YLQKPGQSPQ  50
LLIYEVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCSQSTHVP 100
LTFGQGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK 150
VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE 200
VTHQGLSSPV TKSFNRGEC                                   219
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 149-205 263-323 369-427
22"-96" 149"-205" 263"-323" 369"-427"
Intra-L (C23-C104) 23'-93' 139'-199'
23'"-93'" 139'"-199'"
Inter-H-L (CH1 10-CL 126) 136-219' 136"-219'"
Inter-H-H (h 8, h 11) 228-228" 231-231"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
299, 299"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

licogliflozinum

licogliflozin

(1*S*)-1,5-anhydro-1-*C*-{3-[(2,3-dihydro-1,4-benzodioxin-6-yl)methyl]-4-ethylphenyl}-D-glucitol

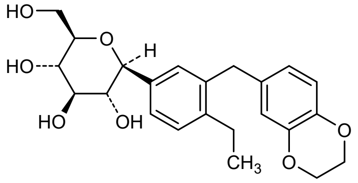
licogliflozine

(1*S*)-1,5-anhydro-1-*C*-{3-[(2,3-dihydro-1,4-benzodioxin-6-yl)méthyl]-4-éthylphényl}-D-glucitol

licogliflozina

(1*S*)-1,5-anhidro-1-*C*-{3-[(2,3-dihidro-1,4-benzodioxin-6-il)metil]-4-etilfenil}-D-glucitol

$C_{23}H_{28}O_7$



lifileucelum

lifileucel

human culture expanded activated autologous T cells for cell-based immunotherapy. The cell substance is a heterogeneous mixture consisting of CD4+ and CD8+ tumor-infiltrating lymphocytes (TIL), derived from isolated metastatic tumor biopsy of patients with metastatic melanoma, and cultured in the presence of feeder cells (irradiated allogeneic mononuclear cells from healthy donors) and human recombinant interleukin 2 (IL-2)/OKT3 anti-CD3 antibody (*muromonab-CD3 (59)(29)*) for T-cell activation.

lifileucel

lymphocytes T humains autologues, activés en culture d'expansion pour immunothérapie cellulaire. Les cellules sont un mélange hétérogène consistant en des lymphocytes T CD4+ et CD8+ infiltrant la tumeur (TIL), dérivés d'une biopsie isolée de la tumeur métastatique de patients avec un mélanome métastatique et mis en culture en présence de cellules nourricières (cellules mononucléaires allogéniques irradiées obtenues à partir de donneurs sains) et d'interleukine 2 (IL2) recombinante humaine/ anticorps OKT3 anti-CD3 (*muromonab-CD3 (59)(29)*) pour l'activation des lymphocytes T.

lifileucel

linfocitos T humanos autólogos activados y expandidos en cultivo para inmunoterapia celular. La substancia celular es una mezcla heterogénea consistente en linfocitos CD4+ y CD8+ infiltrantes de tumor, derivados de una biopsia aislada de tumor metastásico de pacientes con melanoma metastásico, y cultivados en presencia de células *feeder* (células mononucleares alogénicas irradiadas obtenidas de donantes sanos) e interleukina 2 recombinante humana (IL-2)/anticuerpo OKT3 anti-CD3 (*muromonab-CD3 (59)(29)*) para activación de linfocitos T.

linerixibatum

linerixibat

3-({[(3*R*,5*R*)-3-butyl-3-ethyl-7-methoxy-1,1-dioxo-5-phenyl-2,3,4,5-tetrahydro-1*H*-1λ^{6},4-benzothiazepin-8-yl]methyl}amino)pentanedioic acid

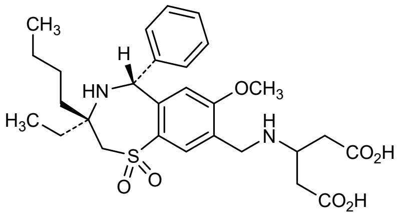
linérixibat

acide 3-({[(3*R*,5*R*)-3-butyl-3-éthyl-7-méthoxy-1,1-dioxo-5-phényl-2,3,4,5-tétrahydro-1*H*-1λ^{6},4-benzothiazépin-8-yl]méthyl}amino)pentanedioïque

linerixibat

ácido 3-({[(3*R*,5*R*)-3-butil-3-etil-7-metoxi-1,1-dioxo-5-fenil-2,3,4,5-tetrahidro-1*H*-1λ^{6},4-benzotiazepin-8-il]metil}amino)pentanodioico

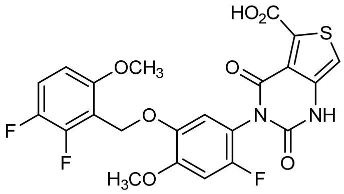
$C_{28}H_{38}N_2O_7S$



linzagolixum

linzagolix	3-{5-[(2,3-difluoro-6-methoxyphenyl)methoxy]-2-fluoro-4-methoxyphenyl}-2,4-dioxo-1,2,3,4-tetrahydrothieno[3,4-*d*]pyrimidine-5-carboxylic acid
linzagolix	acide 3-{5-[(2,3-difluoro-6-méthoxyphényl)méthoxy]-2-fluoro-4-méthoxyphényl}-2,4-dioxo-1,2,3,4-tétrahydrothiéno[3,4-*d*]pyrimidine-5-carboxylique
linzagolix	ácido 3-{5-[(2,3-difluoro-6-metoxifenil)metoxi]-2-fluoro-4-metoxifenil}-2,4-dioxo-1,2,3,4-tetrahidrotieno[3,4-*d*]pirimidina-5-carboxílico

$C_{22}H_{15}F_3N_2O_7S$



livoletidum

livoletide	1,8-anhydro(L-arginyl-L-valyl-L-glutaminyl-L-seryl-L-prolyl-L-α-glutamyl-L-histidyl-L-glutaminyl)
livolétide	1,8-anhydro(L-arginyl-L-valyl-L-glutaminyl-L-séryl-L-prolyl-L-α-glutamyl-L-histidyl-L-glutaminyl)
livoletida	1,8-anhidro(L-arginil-L-valil-L-glutaminil-L-seril-L-prolil-L-α-glutamil-L-histidil-L-glutaminil)

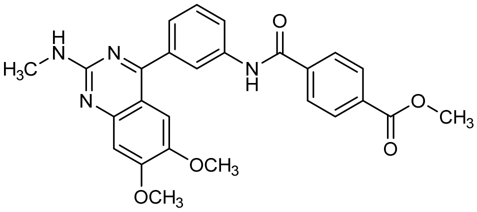
$C_{40}H_{63}N_{15}O_{13}$

lotamilastum

lotamilast	methyl 4-({3-[6,7-dimethoxy-2-(methylamino)quinazolin-4-yl]phenyl}carbamoyl)benzoate
lotamilast	4-({3-[6,7-diméthoxy-2-(méthylamino)quinazolin-4-yl]phényl}carbamoyl)benzoate de méthyle

lotamilast	4-({3-[6,7-dimetoxi-2-(metilamino)quinazolin-4-il]fenil}carbamoil)benzoato de metilo

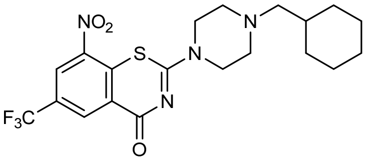
$C_{26}H_{24}N_4O_5$



macozinonum

macozinone	2-[4-(cyclohexylmethyl)piperazin-1-yl]-8-nitro-6-(trifluoromethyl)-4*H*-1,3-benzothiazin-4-one
macozinone	2-[4-(cyclohexylméthyl)pipérazin-1-yl]-8-nitro-6-(trifluorométhyl)-4*H*-1,3-benzothiazin-4-one
macozinona	2-[4-(ciclohexilmetil)piperazin-1-il]-8-nitro-6-(trifluorometil)-4*H*-1,3-benzotiazin-4-ona

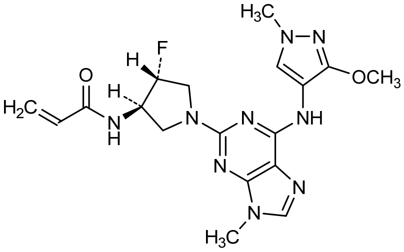
$C_{20}H_{23}F_3N_4O_3S$



mavelertinibum

mavelertinib	*N*-[(3*R*,4*R*)-4-fluoro-1-{6-[(3-methoxy-1-methyl-1*H*-pyrazol-4-yl)amino]-9-methyl-9*H*-purin-2-yl}pyrrolidin-3-yl]prop-2-enamide
mavélertinib	*N*-[(3*R*,4*R*)-4-fluoro-1-{6-[(3-méthoxy-1-méthyl-1*H*-pyrazol-4-yl)amino]-9-méthyl-9*H*-purin-2-yl}pyrrolidin-3-yl]prop-2-énamide
mavelertinib	*N*-[(3*R*,4*R*)-4-fluoro-1-{6-[(3-metoxi-1-metil-1*H*-pirazol-4-il)amino]-9-metil-9*H*-purin-2-il}pirrolidin-3-il]prop-2-enamida

$C_{18}H_{22}FN_9O_2$



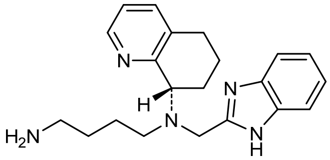
mavilimogenum ralaplasmidum #

mavilimogene ralaplasmid	a DNA plasmid encoding genes for human papilloma virus type 16 (HPV-16) E6 and E7 proteins whose expression is driven by the human cytomegalovirus (hCMV) promoter with the bovine growth hormone (bGH) 3'end gene and bGH gene polyA signal.
mavilimogène ralaplasmide	ADN plasmidique contenant les gènes codant pour les protéines E6 et E7 du virus du papillome humain de type 16 (HPV-16), dont l'expression est dirigée par le promoteur du cytomégalovirus humain (hCMV) avec la région 3'-terminale du gène de l'hormone de croissance bovine (bGH) et le signal poly-A du gène de la bGH
mavilimogén ralaplásmido	un DNA plasmídico que contiene genes que codifican para las proteínas E6 y E7 del virus del papiloma humano tipo 16 (HPV-16), cuya expresión está dirigida por el promotor del citomegalovirus humano (hCMV) con la región 3' terminal del gen de la hormona de crecimiento bovina (bGH) y la señal poli A del gen de bGH

mavorixaforum

mavorixafor	*N*^{1}-[(1*H*-benzimidazol-2-yl)methyl]-*N*^{1}-[(8*S*)-5,6,7,8-tetrahydroquinolin-8-yl]butane-1,4-diamine
mavorixafor	*N*^{1}-[(1*H*-benzimidazol-2-yl)méthyl]-*N*^{1}-[(8*S*)-5,6,7,8-tétrahydroquinoléin-8-yl]butane-1,4-diamine
mavorixafor	*N*^{1}-[(1*H*-benzimidazol-2-il)metil]-*N*^{1}-[(8*S*)-5,6,7,8-tetrahidroquinolein-8-il]butano-1,4-diamina

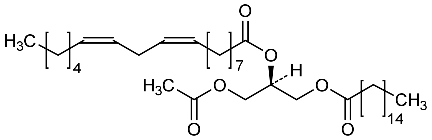
$C_{21}H_{27}N_5$



mosedipimodum

mosedipimod	*rac*-(2*R*)-propane-1,2,3-triyl 1-acetate 3-hexadecanoate 2-[(9*Z*,12*Z*)-octadeca-9,12-dienoate]
mosédipimod	1-acétate, 3-hexadécanoate et 2-[(9*Z*,12*Z*)-octadéca-9,12-diénoate]de *rac*-(2*R*)-propane-1,2,3-triyle
mosedipimod	1-acetato, 3-hexadecanoato y 2-[(9*Z*,12*Z*)-octadeca-9,12-dienoato]de *rac*-(2*R*)-propano-1,2,3-triilo

$C_{39}H_{70}O_6$



and enantiomer
et énantiomère
y enantiómero

nalotimagenum carmaleucelum #

nalotimagene carmaleucel	human culture expanded activated allogeneic T cells for adjunctive immunotherapy. Cells are derived from the haematopoietic stem cell (HSC) donor and are genetically modified *ex vivo* with a non-replicative SFCMM-3 gamma-retroviral vector derived from Moloney murine Leukemia Virus (Mo-MuLV), encoding for a truncated form of the human low affinity nerve growth factor receptor (ΔLNGFR) and the herpes simplex virus thymidine kinase (HSV-TK Mut2). Cells contain a suicide gene in case of graft versus host disease development.
nalotimagène carmaleucel	lymphocytes T humains allogéniques, activés, en culture d'expansion pour immunothérapie adjuvante. Les lymphocytes sont dérivés de cellules souches hématopoïétiques (CSH) d'un donneur et sont génétiquement modifiés *ex vivo* avec un vecteur rétroviral gamma SFCMM-3 non-répliquant dérivé du virus de la leucémie murine de Moloney (Mo-MuLV), codant pour une forme tronquée du récepteur du facteur de croissance nerveuse à faible affinité humain (ΔLNGFR) et la thymidine kinase du virus herpès simplex (HSV-TK Mut2). Les cellules contiennent un gène suicide en cas de développement de réaction du greffon contre l'hôte.
nalotimagén carmaleucel	linfocitos T humanos alogénicos activados y expandidos en cultivo para inmunoterapia adyuvante. Los linfocitos se derivan a partir del donante de las células madre hematopoyéticas (CMH) y se modifican genéticamente *ex vivo* con un vector retroviral gamma SFCMM-3 no replicativo derivado del virus de la leucemia murina de Moloney (Mo-MuLV), que codifica para una forma truncada del receptor para el factor de crecimiento nervioso de baja afinidad humano (ΔLNGFR) y de la timidina quinasa del virus del herpes simplex (HSV-TK Mut2). Las células contienen un gen suicida en caso de que se desarrolle la enfermdad de injerto contra huésped.

netakimabum #

netakimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* IL17A (interleukin 17A, IL-17A)], chimeric and *Homo sapiens* monoclonal antibody; chimeric gamma1 heavy chain (1-455) [VH (*Lama glama* IGHV3S3*01 (80.2%) -(IGHD) -IGHJ3*01 (92.3%)/*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ5*01 (92.9%)) [8.8.18] (1-124) -1-mer seryl linker (125) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (126-223), hinge (224-238), CH2 [M15.1>Y (260), S16>T (262), T18>E (264)] (239-348), CH3 (349-453), CHS (454-455)) (126-455)], (228-215')-disulfide with *Homo sapiens* kappa light chain (1'-216') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (96.9%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimer (234-234'':237-237'')-bisdisulfide

nétakimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* IL17A (interleukine 17A, IL-17A)], anticorps monoclonal chimérique et *Homo sapiens*; chaîne lourde gamma1 chimérique (1-455) [VH (*Lama glama* IGHV3S3*01 (80.2%) -(IGHD) -IGHJ3*01 (92.3%)/*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ5*01 (92.9%)) [8.8.18] (1-124) -1-mer linker séryl (125) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (126-223), charnière (224-238), CH2 [M15.1>Y (260), S16>T (262), T18>E (264)] (239-348), CH3 (349-453), CHS (454-455)) (126-455)], (228-215')-disulfure avec la chaîne légère kappa *Homo sapiens* (1'-216') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (96.9%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dimère (234-234":237-237")-bisdisulfure
netakimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* IL17A (interleukina 17A, IL-17A)], anticuerpo monoclonal quimérico y *Homo sapiens*; cadena pesada gamma1 quimérica (1-455) [VH (*Lama glama* IGHV3S3*01 (80.2%) -(IGHD) -IGHJ3*01 (92.3%)/*Homo sapiens* IGHV3-23*04 -(IGHD) -IGHJ5*01 (92.9%)) [8.8.18] (1-124) -1-mer ligando seril (125) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (126-223), bisagra (224-238), CH2 [M15.1>Y (260), S16>T (262), T18>E (264)] (239-348), CH3 (349-453), CHS (454-455)) (126-455)], (228-215')-disulfuro con la cadena ligera kappa *Homo sapiens* (1'-216') [*Homo sapiens* V-KAPPA (IGKV3-20*01 (96.9%) -IGKJ1*01 (100%)) [7.3.9] (1'-108') -*Homo sapiens* IGKC*01, Km3 A45.1 (154), V101 (192) (109'-215')]; dímero (234-234":237-237")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGGG LVQAGGSLRL SCAASGGTFA TSPMGWLRQA PGKGTEFVAA  50
ISPSGGDRIY ADSVKGRFTI SRDNAGYFIY LQMNSLKPED TAVYYCAVRR 100
RFDGTSYYTG DYDSWGQGTL VTVSSASTKG PSVFPLAPSS KSTSGGTAAL 150
GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL SSVVTVPSSS 200
LGTQTYICNV NHKPSNTKVD KRVEPKSCDK THTCPPCPAP ELLGGPSVFL 250
FPPKPKDTLY ITREPEVTCV VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR 300
EEQYNSTYRV VSVLTVLHQD WLNGKEYKCK VSNKALPAPI EKTISKAKGQ 350
PREPQVYTLP PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK 400
TTPPVLDSDG SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS 450
LSPGK                                              455
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Light chain / Chaîne légère / Cadena ligera

```
EIVLTQSPGT LSLSPGERAT LSCRASQSVS SSYLAWYQQK PGQAPRLLIY  50
DASSRATGIP DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYSYSPVTFG 100
QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQWK 150
VDNALQSGNS QESVTEQDSK DSTYSLSSTL TLSKADYEKH KVYACEVTHQ 200
GLSSPVTKSF NRGEC                                   215
```

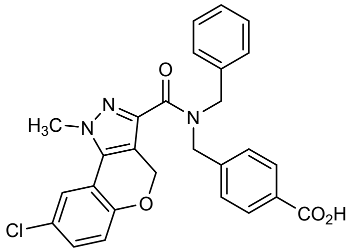
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 152-208 269-329 375-433
22"-96" 152"-208" 269"-329" 375"-433"
Intra-L (C23-C104) 23'-89' 135'-195'
23'''-89''' 135'''-195'''
Inter-H-L (h 5-CL 126) 228-215' 228"-215'''
Inter-H-H (h 11, h 14) 234-234" 237-237"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
305, 305"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

nidufexorum

nidufexor	4-[(*N*-benzyl-8-chloro-1-methyl-1,4-dihydro[1]benzopyrano[4,3-*c*]pyrazole-3-carboxamido)methyl]benzoic acid
nidufexor	acide 4-[(*N*-benzyl-8-chloro-1-méthyl-1,4-dihydro[1]benzopyrano[4,3-*c*]pyrazole-3-carboxamido)méthyl]benzoïque
nidufexor	ácido 4-[(*N*-bencil-8-cloro-1-metil-1,4-dihidro[1]benzopirano[4,3-*c*]pirazol-3-carboxamido)metil]benzoico

$C_{27}H_{22}ClN_3O_4$



onfekafuspum alfa #

onfekafusp alfa	immunoglobulin single-chain variable fragment anti-(human fibronectin ED-B domain) (1-236), with a GDGSSGGSGGAS linker (117-128) between the VH and VL regions, fused, via a EF($S_4G)_3$ linker (237-253), to human tumor necrosis factor (TNF) soluble form (254-410), non-covalent trimer, produced in Chinese hamster ovary (CHO) cells, glycoform alfa : scFv-TNF chain (1-410) [*Homo sapiens* VH (IGHV3-23*01 (94.9%)-(IGHD) -IGHJ4*01 (100%)) [8.8.9](1-116) -12-mer linker(117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.8%)-IGKJ1*01 (100%))[7.3.9] (129-236) -17-mer EF(SSSSG)3 linker (237-253)-*Homo sapiens* TNF (Pr77-233)(254-410)], non-covalent trimer
onfékafusp alfa	immunoglobuline à chaîne unique Fragment variable (scFv), anti-(domaine ED-B de la fibronectine humaine) (1-236), avec un linker GDGSSGGSGGAS (117-128) entre les régions VH et VL, fusionné, via un linker EF($S_4G)_3$ (237-253), à la forme soluble du facteur de nécrose tumorale (TNF) humain (254-410), trimère non covalent, produit par des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa: chaîne scFv-TNF (1-410) [*Homo sapiens* VH (IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (100%))[8.8.9] (1-116) -12-mer linker (117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.8%) -IGKJ1*01 (100%))[7.3.9] (129-236) -17-mer EF(SSSSG)3 linker (237-253) -*Homo sapiens* TNF (Pr77-233) (254-410)], trimère non-covalent

onfekafusp alfa

inmunoglobulina con la cadena única Fragmento variable (scFv), anti-(dominio ED-B de la fibronectina humana) (1-236), con un ligando GDGSSGGSGGAS (117-128) entre las regiones VH y VL, fusionado, a través de un enlace EF(S_4G)$_3$ (237-253), con la forma soluble del factor de necrosis tumoral (TNF) humano (254-410), trímero no covalente, producido por las células ováricas de hamsters chinos (CHO), glicoforma alfa:
cadena scFv-TNF (1-410) [*Homo sapiens* VH (IGHV3-23*01 (94.9%) -(IGHD) -IGHJ4*01 (100%))[8.8.9] (1-116) -12-mer ligando (117-128) -*Homo sapiens* V-KAPPA (IGKV3-20*01 (94.8%) -IGKJ1*01 (100%))[7.3.9] (129-236) -17-mer EF(SSSSG)3 ligando (237-253) -*Homo sapiens* TNF (Pr77-233) (254-410)], trímero no covalente

Chain / Chaîne / Cadena scFv-TNF

```
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SFSMSWVRQA PGKGLEWVSS 50
ISGSSGTTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKPF 100
PYFDYWGQGT LVTVSSGDGS SGGSGGASEI VLTQSPGTLS LSPGERATLS 150
CRASQSVSSS FLAWYQQKPG QAPRLLIYYA SSRATGIPDR FSGSGSGTDF 200
TLTISRLEPE DFAVYYCQQT GRIPPTFGQG TKVEIKEFSS SSGSSSSGSS 250
SSGVRSSSRT PSDKPVAHVV ANPQAEGQLQ WLNRRANALL ANGVELRDNQ 300
LVVPSEGLYL IYSQVLFKGQ GCPSTHVLLT HTISRIAVSY QTKVNLLSAI 350
KSPCQRETPE GAEAKPWYEP IYLGGVFQLE KGDRLSAEIN RPDYLDFAES 400
GQVYFGIIAL                                             410
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 151-217
Intra-TNF 322-354

Glycosylation site (O) / Site de glycosylation (O) / Posición de glicosilación (O)
Ser-257
CHO-type O-glycans / O-glycanes de type CHO / O-glicanos de tipo CHO

onvatilimabum #
onvatilimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* VSIR (V-set immunoregulatory receptor, C10orf54, chromosome 10 orf54, B7H5, B7-H5, PDCD1 homolog, PD-1H, stress induced secreted protein 1, SISP1, V-domain Ig suppressor of T cell activation, VISTA)], human monoclonal antibody;
gamma1 heavy chain (1-450) [*Homo sapiens* VH (IGHV1-69*01 (100.00%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), hinge (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (92.6%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(223'-214')]; dimer (229-229'':232-232'')-bisdisulfide

onvatilimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* VSIR (récepteur immunorégulateur du V-set, C10orf54, orf54 du chromosome 10, B7H5, B7-H5, homologue du PDCD1, PD-1H, protéine 1 secrétée induite par le stress, SISP1, suppresseur d'activation de cellule T du V-set Ig, VISTA)], anticorps monoclonal humain;

chaîne lourde gamma1 (1-450) [*Homo sapiens* VH (IGHV1-69*01 (100.00%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), charnière (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (92.6%) -IGKJ1*01(100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(223'-214')]; dimère (229-229'':232-232'')-bisdisulfure

onvatilimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* VSIR (receptor inmunoregulador del V-set, C10orf54, orf54 del cromosoma 10, B7H5, B7-H5, homólogo del PDCD1, PD-1H, proteína 1 secretada inducida por el estrés, SISP1, supresor de la activación de célula T del V-set Ig, VISTA)], anticuerpo monoclonal humano;
cadena pesada gamma1 (1-450) [*Homo sapiens* VH (IGHV1-69*01 (100.00%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), bisagra (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (92.6%) -IGKJ1*01(100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (223'-214')]; dímero (229-229'':232-232'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLVQSGAE VKKPGSSVKV SCKASGGTFS SYAISWVRQA PGQGLEWMGG  50
IIPIFGTANY AQKFQGRVTI TADESTSTAY MELSSLRSED TAVYYCARSS 100
YGWSYEFDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQSID TRLNWYQQKP GKAPKLLIYS  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SAYNPITFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                       214
```

Post-translational modifications
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22''-96'' 147''-203'' 264''-324'' 370''-428''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 223-214' 223''-214'''
Inter-H-H (h 11, h 14) 229-229'' 232-232''

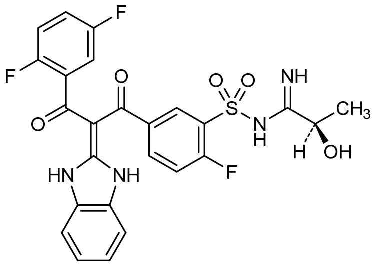
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

opigolixum
opigolix

(2*R*)-*N*-{5-[3-(2,5-difluorophenyl)-2-(1,3-dihydro-2*H*-benzimidazol-2-ylidene)-3-oxopropanoyl]-2-fluorobenzene-1-sulfonyl}-2-hydroxypropanimidamide

opigolix	(2*R*)-*N*-{5-[3-(2,5-difluorophényl)-2-(1,3-dihydro-2*H*-benzimidazol-2-ylidène)-3-oxopropanoyl]-2-fluorobenzène-1-sulfonyl}-2-hydroxypropanimidamide
opigolix	(2*R*)-*N*-{5-[3-(2,5-difluorofenil)-2-(1,3-dihidro-2*H*-benzimidazol-2-ilideno)-3-oxopropanoil]-2-fluorobenceno-1-sulfonil}-2-hidroxipropanimidamida

$C_{25}H_{19}F_3N_4O_5S$



opinerceptum #

opinercept	human tumor necrosis factor receptor-2 extracellular domain (1-235) fused to a fragment of immunoglobulin G1 consisting of the Fc portion and hinge region (236-467), dimer, produced in Chinese hamster ovary (CHO) cells, glycosylated
opinercept	domaine extracellulaire du récepteur 2 du facteur de nécrose tumorale humain (1-235) fusionné à un fragment d'immunoglobuline G1 constitué du fragment Fc et de la région charnière (236-467), dimère, produit par des cellules ovariennes de hamsters chinois (CHO), glycosylé
opinercept	dominio extracelular del receptor 2 del factor de necrosis tumoral humano (1-235) fusionado con un fragmento de inmunoglobulina G1 constituida por el fragmento Fc y la región bisagra (236-467), dímero, producido por las células ováricas de hamsters chinos (CHO), glicosilado

```
LPAQVAFTPY APEPGSTCRL REYYDQTAQM CCSKCSPGQH AKVFCTKTSD 50
TVCDSCEDST YTQLWNWVPE CLSCGSRCSS DQVETQACTR EQNRICTCRP 100
GWYCALSKQE GCRLCAPLRK CRPGFGVARP GTETSDVVCK PCAPGTFSNT 150
TSSTDICRPH QICNVVAIPG NASMDAVCTS TSPTRSMAPG AVHLPQPVST 200
RSQHTQPTPE PSTAPSTSFL LPMGPSPPAE GSTGDEPKSC DKTHTCPPCP 250
APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD 300
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA 350
PIEKTISKAK GQPREPQVYT LPPSRDELTK NQVSLTCLVK GFYPSDIAVE 400
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE 450
ALHNHYTQKS LSLSPGK                                     467
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
intra-chain: 18-31 32-45 35-53 56-71 74-88 78-96 98-104 112-121
115-139 142-157 163-178 281-341 387-445
inter-chain: 240-240' 246-246' 249-249'

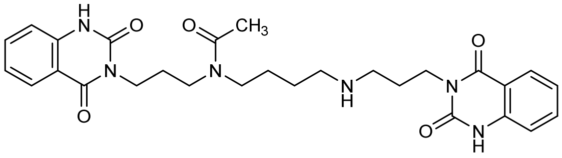
Glycosylation sites (N) / Sites de glycosylation (N) / Posiciones de glicosilación (N)
Asn-149 Asn-171 Asn-317

Glycosylation sites (O) / Sites de glycosylation (O) / Posiciones de glicosilación (O)
Thr-8 Thr-184 Ser-199 Thr-200 Ser-202 Thr-205 Thr-208 Ser-212
Thr-213 Ser-216 Thr-217 Ser-218 Ser-226 Ser-232 Thr-233 Thr-243

otaplimastatum

otaplimastat	*N*-[3-(2,4-dioxo-1,4-dihydroquinazolin-3(2*H*)-yl)propyl]-*N*-(4-{[3-(2,4-dioxo-1,4-dihydroquinazolin-3(2*H*)-yl)propyl]amino}butyl)acetamide
otaplimastat	*N*-[3-(2,4-dioxo-1,4-dihydroquinazolin-3(2*H*)-yl)propyl]-*N*-(4-{[3-(2,4-dioxo-1,4-dihydroquinazolin-3(2*H*)-yl)propyl]amino}butyl)acetamide
otaplimastat	*N*-[3-(2,4-dioxo-1,4-dihidroquinazolin-3(2*H*)-il)propil]-*N*-(4-{[3-(2,4-dioxo-1,4-dihidroquinazolin-3(2*H*)-il)propil]amino}butil)acetamida

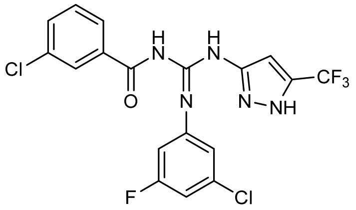
$C_{28}H_{34}N_6O_5$



parimifasorum

parimifasor	3-chloro-*N*-[(3-chloro-5-fluoroanilino){[5-(trifluoromethyl)-1*H*-pyrazol-3-yl]amino}methylidene]benzamide
parimifasor	3-chloro-*N*-[(3-chloro-5-fluoroanilino){[5-(trifluorométhyl)-1*H*-pyrazol-3-yl]amino}méthylidène]benzamide
parimifasor	3-cloro-*N*-[(3-cloro-5-fluoroanilino){[5-(trifluorometil)-1*H*-pirazol-3-il]amino}metilideno]benzamida

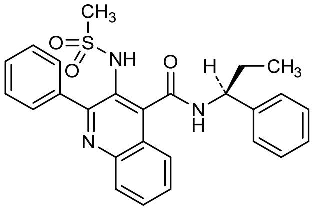
$C_{18}H_{11}Cl_2F_4N_5O$



pavinetantum

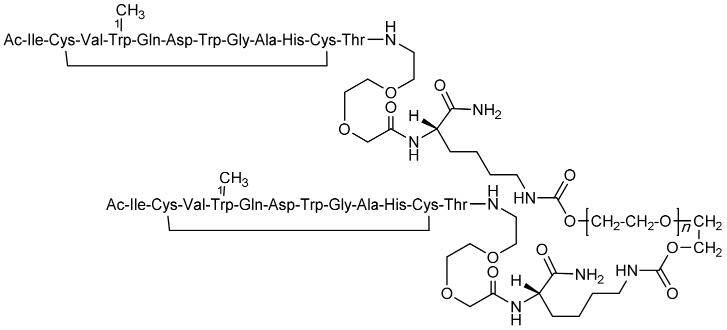
pavinetant	3-(methanesulfonamido)-2-phenyl-*N*-[(1*S*)-1-phenylpropyl]quinoline-4-carboxamide
pavinétant	3-(méthanesulfonamido)-2-phényl-*N*-[(1*S*)-1-phénylpropyl]quinoléine-4-carboxamide
pavinetant	3-(metanosulfonamido)-2-fenil-*N*-[(1*S*)-1-fenilpropil]quinoleína-4-carboxamida

$C_{26}H_{25}N_{3}O_{3}S$



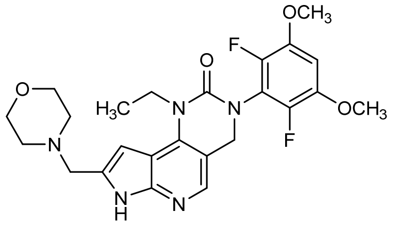
pegcetacoplanum	
pegcetacoplan	*O*,*O*'-bis[(S^{2},S^{12}-cyclo{*N*-acetyl-L-isoleucyl-L-cysteinyl-L-valyl-1-methyl-L-tryptophyl-L-glutaminyl-L-α-aspartyl-L-tryptophylglycyl-L-alanyl-L-histidyl-L-arginyl-L-cysteinyl-L-threonyl-2-[2-(2-aminoethoxy)ethoxy]acetyl-L-lysinamide})-$N^{6.15}$-carbonyl]polyethylene glycol (n = 800-1100)
pegcétacoplan	*O*,*O*'-bis[(S^{2},S^{12}-cyclo{*N*-acétyl-L-isoleucyl-L-cystéinyl-L-valyl-1-méthyl-L-tryptophyl-L-glutaminyl-L-α-aspartyl-L-tryptophylglycyl-L-alanyl-L-histidyl-L-arginyl-L-cystéinyl-L-thréonyl-2-[2-(2-aminoéthoxy)éthoxy]acétyl-L-lysinamide})-$N^{6.15}$-carbonyl]polyéthylène glycol (n = 800-1100)
pegcetacoplán	*O*,*O*'-bis[(S^{2},S^{12}-ciclo{*N*-acetil-L-isoleucil-L-cisteinil-L-valil-1-metil-L-triptofil-L-glutaminil-L-α-aspartil-L-triptofilglicil-L-alanil-L-histidil-L-arginil-L-cisteinil-L-treonil-2-[2-(2-aminoetoxi)etoxi]acetil-L-lisinamida})-$N^{6.15}$-carbonil]polietileno glicol (n = 800-1100)

$C_{170}H_{248}N_{50}O_{47}S_{4}$



pemigatinibum	
pemigatinib	3-(2,6-difluoro-3,5-dimethoxyphenyl)-1-ethyl-8-[(morpholin-4-yl)methyl]-1,3,4,7-tetrahydro-2*H*-pyrrolo[3',2':5,6]pyrido[4,3-*d*]pyrimidin-2-one
pémigatinib	3-(2,6-difluoro-3,5-diméthoxyphényl)-1-éthyl-8-[(morpholin-4-yl)méthyl]-1,3,4,7-tétrahydro-2*H*-pyrrolo[3',2':5,6]pyrido[4,3-*d*]pyrimidin-2-one
pemigatinib	3-(2,6-difluoro-3,5-dimetoxifenil)-1-etil-8-[(morfolin-4-il)metil]-1,3,4,7-tetrahidro-2*H*-pirrolo[3',2':5,6]pirido[4,3-*d*]pirimidin-2-ona

$C_{24}H_{27}F_2N_5O_4$



praconasum #

praconase

L-seryl (1)-[mono-ADP-ribosyltransferase C3 (exoenzyme C3, EC=2.4.2.-) of *Clostridium botulinum* D phage (2-212)] fusion protein with an artificial permeability-conferring C-terminal 19-peptide (213-231), produced in *Escherichia coli*

praconase

L-séryl (1)-[mono-ADP-ribosyltransférase C3 de phage de *Clostridium botulinum* de type D (exoenzyme C3, EC=2.4.2.-)], fusionnée par l'extrémité C-terminale à un peptide conférant une perméabilité artificielle (213-231), produite par *Escherichia coli*

praconasa

L-seril (1)-[mono-ADP-ribosiltransferasa C3 de phage de *Clostridium botulinum* de tipo D (exoenzima C3, EC=2.4.2.-) (2-212)], fusionada con la extremidad C-terminal a un péptido que confiere una permeabilidad artificial (213-231), producido por *Escherichia coli*

```
SAYSNTYQEF TNIDQAKAWG NAQYKKYGLS KSEKEAIVSY TKSASEINGK 50
LRQNKGVING FPSNLIKQVE LLDKSFNKMK TPENIMLFRG DDPAYLGTEF 100
QNTLLNSNGT INKTAFEKAK AKFLNKDRLE YGYISTSLMN VSQFAGRPII 150
TKFKVAKGSK AGYIDPISAF AGQLEMLLPR HSTYHIDDMR LSSDGKQIII 200
TATMMGTAIN PKEFVMNPAN AQGRHTPGTR L                     231
```

ravagalimabum #

ravagalimab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CD40 (tumor necrosis factor super family member 5, TNFRSF5)], humanized monoclonal antibody;
gamma1 heavy chain (1-446) [humanized VH (*Homo sapiens* IGHV3-48*01 (89.8%) -(IGHD)-IGHJ6*01 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), hinge (215-229), CH2 L1.3>A (233), L1.2>A (234), T14>Q (249) (230-339), CH3 E12 (355), M14 (357), M107>L (427) (340-444), CHS (445-446)) (117-446)], (219-220')-disulfide with kappa light chain (1'-220') [humanized V-KAPPA (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01, Km3 A45.1 (159), V101 (197) (114'-220')]; dimer (225-225":228-228")-bisdisulfide

ravagalimab

immunoglobuline G1-kappa, anti-[*Homo sapiens* CD40 (membre 5 de la superfamille des récepteurs du TNF, TNFRSF5)], anticorps monoclonal humanisé;

chaîne lourde gamma1 (1-446) [VH humanisé (*Homo sapiens* IGHV3-48*01 (89.8%) -(IGHD)-IGHJ6*01 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), charnière (215-229), CH2 L1.3>A (233), L1.2>A (234), T14>Q (249) (230-339), CH3 E12 (355), M14 (357), M107>L (427) (340-444), CHS (445-446)) (117-446)], (219-220')-disulfure avec la chaîne légère kappa (1'-220') [V-KAPPA humanisé (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01, Km3 A45.1 (159), V101 (197) (114'-220')]; dimère (225-225":228-228")-bisdisulfure

ravagalimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* CD40 (miembro 5 de la superfamilia de los receptores del TNF, TNFRSF5)], anticuerpo monoclonal humanizado;
cadena pesada gamma1 (1-446) [VH humanizado (*Homo sapiens* IGHV3-48*01 (89.8%) -(IGHD)-IGHJ6*01 (100%)) [8.8.9] (1-116) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (213) (117-214), bisagra (215-229), CH2 L1.3>A (233), L1.2>A (234), T14>Q (249) (230-339), CH3 E12 (355), M14 (357), M107>L (427) (340-444), CHS (445-446)) (117-446)], (219-220')-disulfuro con la cadena ligera kappa (1'-220') [V-KAPPA humanizado (*Homo sapiens* IGKV4-1*01 (89.1%) -IGKJ2*01 (100%)) [12.3.9] (1'-113') -*Homo sapiens* IGKC*01, Km3 A45.1 (159), V101 (197) (114'-220')]; dímero (225-225":228-228")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS DYGMNWVRQA PGKGLEWIAY  50
ISSGRGNIYY ADTVKGRFTI SRDNAKNSLY LQMNSLRAED TAVYYCARSW 100
GYFDVWGQGT TVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP 150
EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN 200
VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PEAAGGPSVF LFPPKPKDQL 250
MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL 350
PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 400
GSFFLYSKLT VDKSRWQQGN VFSCSVLHEA LHNHYTQKSL SLSPGK      446
```

Light chain / Chaîne légère / Cadena ligera

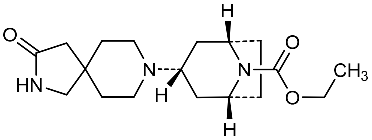
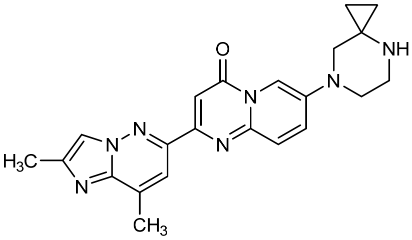
```
DIVMTQSPDS LAVSLGERAT INCKSSQSLL NRGNQKNYLT WFQQKPGQPP  50
KLLIYWASTR ESGVPDRFSG SGSGTDFTLT ISSLQAEDVA VYYCQNDYTY 100
PLTFGQGTKL EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA 150
KVQWKVDNAL QSGNSQESVT EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC 200
EVTHQGLSSP VTKSFNRGEC                                  220
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 143-199 260-320 366-424
22"-96" 143"-199" 260"-320" 366"-424"
Intra-L (C23-C104) 23'-94' 140'-200'
23'''-94''' 140'''-200'''
Inter-H-L (h 5-CL 126) 219-220' 219"-220'''
Inter-H-H (h 11, h 14) 225-225" 228-228"

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
296, 296"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

rebisufligenum etisparvovecum #
rebisufligene etisparvovec

a non-replicating, recombinant, self-complementary adeno-associated virus serotype 9 (scAAV9) vector, expressing the human N-sulfoglucosamine sulfohydrolase (hSGSH) cDNA, under the control of a murine small nuclear RNA promoter U1a.

rébisufligène étisparvovec	vecteur viral adéno-associé de sérotype 9 non-répliquant, recombinant et autocomplémentaire (scAAV9), contenant l'ADN circulaire de la N-sulfoglucosamine sulfohydrolase humaine (hSGSH), sous le contrôle d'un promoteur U1a de petit ARN nucléaire murin.
rebisufligén etisparvovec	un vector de virus adeno-asociado serotipo 9 no-replicativo, recombinante, y auto-complementario, que expresa el cDNA de la N-sulfoglucosamina sulfohidrolasa humana, bajo el control de un promotor U1a de RNA nuclear pequeño murino.
revosimelinum	
revosimeline	ethyl (1*R*,3*r*,5*S*)-3-(3-oxo-2,8-diazaspiro[4.5]decan-8-yl)-8-azabicyclo[3.2.1]octane-8-carboxylate
révosiméline	(1*R*,3*r*,5*S*)-3-(3-oxo-2,8-diazaspiro[4.5]décan-8-yl)-8-azabicyclo[3.2.1]octane-8-carboxylate d'éthyle
revosimelina	(1*R*,3*r*,5*S*)-3-(3-oxo-2,8-diazaspiro[4.5]decan-8-il)-8-azabiciclo[3.2.1]octano-8-carboxilato de etilo
	$C_{18}H_{29}N_3O_3$ 
risdiplamum	
risdiplam	7-(4,7-diazaspiro[2.5]octan-7-yl)-2-(2,8-dimethylimidazo[1,2-*b*]pyridazin-6-yl)-4*H*-pyrido[1,2-*a*]pyrimidin-4-one
risdiplam	7-(4,7-diazaspiro[2.5]octan-7-yl)-2-(2,8-diméthylimidazo[1,2-*b*]pyridazin-6-yl)-4*H*-pyrido[1,2-*a*]pyrimidin-4-one
risdiplam	7-(4,7-diazaspiro[2.5]octan-7-il)-2-(2,8-dimetilimidazo[1,2-*b*]piridazin-6-il)-4*H*-pirido[1,2-*a*]pirimidin-4-ona
	$C_{22}H_{23}N_7O$ 
roblitinibum	
roblitinib	*N*-{5-cyano-4-[(2-methoxyethyl)amino]pyridin-2-yl}-7-formyl-6-[(4-methyl-2-oxopiperazin-1-yl)methyl]-3,4-dihydro-1,8-naphthyridine-1(2*H*)-carboxamide

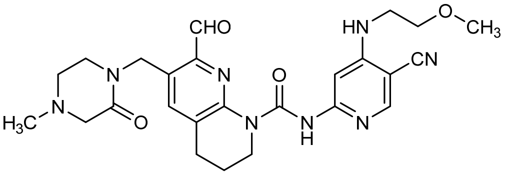
roblitinib

N-{5-cyano-4-[(2-méthoxyéthyl)amino]pyridin-2-yl}-7-formyl-6-[(4-méthyl-2-oxopipérazin-1-yl)méthyl]-3,4-dihydro-1,8-naphthyridine-1(2*H*)-carboxamide

roblitinib

N-{5-ciano-4-[(2-metoxietil)amino]piridin-2-il}-7-formil-6-[(4-metil-2-oxopiperazin-1-il)metil]-3,4-dihidro-1,8-naftiridina-1(2*H*)-carboxamida

$C_{25}H_{30}N_8O_4$



romilkimabum #

romilkimab

immunoglobulin G4-kappa, anti-[*Homo sapiens* IL13 (interleukin 13, IL-13)] and anti-[*Homo sapiens* IL4 (interleukin 4, IL-4)], chimeric and humanized monoclonal antibody, bispecific, tetravalent; gamma1 heavy chain (1-577) [VH anti-IL13 (*Mus musculus* IGHV2-6-7*01 (83.50%) -(IGHD) -IGHJ4*01 (93.8%)/*Homo sapiens* IGHV2-26*01 (59.6%) -(IGHD) -IGHJ1*01 (90.9%)) [8.7.12] (1-118) -10-mer linker bis(tetraglycyl-seryl) (119-128) -VH anti-IL4 (*Mus musculus* IGHV1S127*01 (81.6%) -(IGHD) -IGHJ1*01 (87.5%)/*Homo sapiens* IGHV1-46*01 (68.4%) -(IGHD) -IGHJ4*01 (86.7%)) [8.8.16] (129-251) -*Homo sapiens* IGHG4*01 (CH1 (252-349), hinge 1-12, S10>P (359) (350-361), CH2 L1.2>E (366) (362-471), CH3 (472-576), CHS K>del (577)) (252-577)]; (265-335')-disulfide with kappa light chain (1'-335') [V-KAPPA anti-IL13 (*Mus musculus* IGKV3-10*01 (92.90%) -IGKJ1*01 (100%)/*Homo sapiens*) IGKV4-1*01 (71.9%) -IGKJ4*01 (90.9%)) [10.3.9] (1'-111') -10-mer linker bis(tetraglycyl-seryl) (112'-121') -humanized V-KAPPA anti-IL4 (*Homo sapiens* IGKV1-12*01 (76.8%) -IGKJ2*02 (90.9%)) [6.3.9] (122'-228') -*Homo sapiens* IGKC*01, Km3 A45.1 (274), V101 (312) (229'-335')]; dimer (357-357":360-360")-bisdisulfide

romilkimab

immunoglobuline G4-kappa, anti-[*Homo sapiens* IL13 (interleukine 13, IL-13)] et anti-[*Homo sapiens* IL4 (interleukine 4, IL-4)], anticorps monoclonal chimérique et humanisé, bispécifique, tétravalent; chaîne lourde gamma1 (1-577) [VH anti-IL13 (*Mus musculus* IGHV2-6-7*01 (83.50%) -(IGHD) -IGHJ4*01) (93.8%)/*Homo sapiens* IGHV2-26*01 (59.6%) -(IGHD) -IGHJ1*01 (90.9%)) [8.7.12] (1-118) -10-mer linker bis(tétraglycyl-séryl) (119-128) -VH anti-IL4 (*Mus musculus* IGHV1S127*01 (81.6%) -(IGHD) -IGHJ1*01 (87.5%)/*Homo sapiens* IGHV1-46*01 (68.4%) -(IGHD) -IGHJ4*01 (86.7%)) [8.8.16] (129-251) -*Homo sapiens* IGHG4*01 (CH1 (252-349), charnière 1-12, S10>P (359) (350-361), CH2 L1.2>E (366) (362-471), CH3 (472-576), CHS K>del (577)) (129-577)]; (265-335')-disulfure avec la chaîne légère kappa (1'-335') [V-KAPPA anti-IL13 (*Mus musculus* IGKV3-10*01 (92.90%) -IGKJ1*01) (100%)/*Homo sapiens*) IGKV4-1*01 (71.9%) -IGKJ4*01 (90.9%)) [10.3.9] (1'-111') -10-mer linker bis(tétraglycyl-séryl) (112'-121') -V-KAPPA anti-IL4 humanisé (*Homo sapiens* IGKV1-12*01 (76.8%) -IGKJ2*02 (90.9%)) [6.3.9] (122'-228') -*Homo sapiens* IGKC*01,Km3 A45.1 (274), V101 (312) (229'-335')]; dimère (357-357":360-360")-bisdisulfure romilkimab

inmunoglobulina G4-kappa, anti-[*Homo sapiens* IL13 (interleukina 13, IL-13)] y anti-[*Homo sapiens* IL4 (interleukina 4, IL-4)], anticuerpo monoclonal quimérico y humanizado, biespecífico, tetravalente;
cadena pesada gamma1 (1-577) [VH anti-IL13 (*Mus musculus* IGHV2-6-7*01 (83.50%) -(IGHD) -IGHJ4*01) (93.8%)/*Homo sapiens* IGHV2-26*01 (59.6%) -(IGHD) -IGHJ1*01 (90.9%)) [8.7.12] (1-118) -10-mer ligando bis(tetraglicil-seril) (119-128) -VH anti-IL4 (*Mus musculus* IGHV1S127*01 (81.6%) -(IGHD) -IGHJ1*01 (87.5%)/*Homo sapiens* IGHV1-46*01 (68.4%) -(IGHD) -IGHJ4*01 (86.7%)) [8.8.16] (129-251) -*Homo sapiens* IGHG4*01 (CH1 (252-349), bisagra 1-12, S10>P (359) (350-361), CH2 L1.2>E (366) (362-471), CH3 (472-576), CHS K>del (577)) (129-577)]; (265-335')-disulfuro con la cadena ligera kappa (1'-335') [V-KAPPA anti-IL13 (*Mus musculus* IGKV3-10*01 (92.90%) -IGKJ1*01) (100%)/*Homo sapiens*) IGKV4-1*01 (71.9%) -IGKJ4*01 (90.9%)) [10.3.9] (1'-111') -10-mer ligando bis(tetraglicil-seril) (112'-121') -V-KAPPA anti-IL4 humanizado (*Homo sapiens* IGKV1-12*01 (76.8%) -IGKJ2*02 (90.9%)) [6.3.9] (122'-228') -*Homo sapiens* IGKC*01,Km3 A45.1 (274), V101 (312) (229'-335')]; dímero (357-357":360-360")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLKESGPG LVAPGGSLSI TCTVSGFSLT DSSINWVRQP PGKGLEWLGM  50
IWGDGRIDYA DALKSRLSIS KDSSKSQVFL EMTSLRTDDT ATYYCARDGY 100
FPYAMDFWGQ GTSVTVSSGG GGSGGGGSQV QLQQSGPELV KPGASVKISC 150
KASGYSFTSY WIHWIKQRPG QGLEWIGMID PSDGETRLNQ RFQGRATLTV 200
DESTSTAYMQ LRSPTSEDSA VYYCTRLKEY GNYDSFYFDV WGAGTLVTVS 250
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG 300
VHTFPAVLQS SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE 350
SKYGPPCPPC PAPEFEGGPS VFLFPPKPKD TLMISRTPEV TCVVVDVSQE 400
DPEVQFNWYV DGVEVHNAKT KPREEQFNST YRVVSVLTVL HQDWLNGKEY 450
KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT KNQVSLTCLV 500
KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE 550
GNVFSCSVMH EALHNHYTQK SLSLSLG                         577
```

Light chain / Chaîne légère / Cadena ligera

```
DIVLTQSPAS LAVSLGQRAT ISCRASESVD SYGQSYMHWY QQKAGQPPKL  50
LIYLASNLES GVPARFSGSG SRTDFTLTID PVQAEDAATY YCQQNAEDSR 100
TFGGGTKLEI KGGGGSGGGG SDIQMTQSPA SLSVSVGDTI TLTCHASQNI 150
DVWLSWFQQK PGNIPKLLIY KASNLHTGVP SRFSGSGSGT GFTLTISSLQ 200
PEDIATYYCQ QAHSYPFTFG GGTKLEIKRT VAAPSVFIFP PSDEQLKSGT 250
ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL 300
TLSKADYEKH KVYACEVTHQ GLSSPVTKSF NRGEC                335
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

```
Intra-H (C23-C104)   22-95     150-224     278-334     392-452     498-556
                     22"-95"   150"-224"   278"-334"   392"-452"   498"-556"
Intra-L (C23-C104)   23'-92'   144'-209'   255'-315'
                     23'"-92'" 144'"-209'" 255'"-315'"
Inter-H-L (CH1 10-CL 126)   265-335'   265"-335'"
Inter-H-H (h 8, h 11)       357-357"   360-360"
```

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
428, 428"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados.

samrotamabum #
samrotamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* LRRC15 (leucine-rich repeat-containing member 15, leucine-rich repeat member induced by beta-amyloid homolog, LIB)], humanized and chimeric monoclonal antibody;
gamma1 heavy chain (1-450) [humanized VH (*Homo sapiens* IGHV1-2*02 (77.6%) -(IGHD) -IGHJ5*01 (86.7%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), hinge (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain chimeric (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01,Km3 A45.1 (153), V101 (191)(108'-214')]; dimer (229-229":232-232")-bisdisulfide

samrotamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* LRRC15 (membre 15 contenant des répétitions riches en leucine, membre des répétitions riches en leucine induit par l'homologue bêta-amyloïde, LIB)], anticorps monoclonal humanisé et chimérique; chaîne lourde gamma1 (1-450) [VH humanisé (*Homo sapiens* IGHV1-2*02 (77.60%) -(IGHD) -IGHJ5*01 (86.7%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), charnière (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa chimérique (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimère (229-229'':232-232'')-bisdisulfure
samrotamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* LRRC15 (miembro 15 que contiene las repeticiones ricas en leucina, miembro de las repeticiones ricas en leucina inducido por el homólogo beta-amiloide, LIB)], anticuerpo monoclonal humanizado y quimérico; cadena pesada gamma1 (1-450) [VH humanizado (*Homo sapiens* IGHV1-2*02 (77.60%) -(IGHD) -IGHJ5*01 (86.7%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), bisagra (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa quimérica (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGASVKV SCKASGYKFS SYWIEWVKQA PGQGLEWIGE  50
ILPGSDTTNY NEKFKDRATF TSDTSINTAY MELSRLRSDD TAVYYCARDR 100
GNYRAWFGYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GGAVKFLIYY  50
TSRLHSGVPS RFSGSGSGTD YTLTISSLQP EDFATYFCQQ GEALPWTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104)	22-96	147-203	264-324	370-428
	22''-96''	147''-203''	264''-324''	370''-428''
Intra-L (C23-C104)	23'-88'	134'-194'		
	23'''-88'''	134'''-194'''		
Inter-H-L (h 5-CL 126)	223-214'	223''-214'''		
Inter-H-H (h 11, h 14)	229-229''	232-232''		

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
G0F, G1F

C-terminal lysine clipping:
H CHS K2: 450, 450''

samrotamabum vedotinum #

samrotamab vedotin	immunoglobulin G1-kappa, anti-[*Homo sapiens* LRRC15 (leucine-rich repeat-containing protein 15, leucine-rich repeat induced by beta-amyloid homolog, LIB)], humanized and chimeric monoclonal antibody conjugated to auristatin E; gamma1 heavy chain (1-450) [humanized VH (*Homo sapiens* IGHV1-2*02 (77.6%) -(IGHD) -IGHJ5*01 (86.7%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), hinge (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfide with kappa light chain chimeric (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01,Km3 A45.1 (153), V101 (191)(108'-214')]; dimer (229-229'':232-232'')-bisdisulfide; conjugated, on an average of 2 cysteinyl, to monomethylauristatin E (MMAE), via a cleavable maleimidocaproyl-valyl-citrullinyl-p-aminobenzyloxycarbonyl (mc-val-cit-PABC) type linker For the *vedotin* part, please refer to the document *"INN for pharmaceutical substances: Names for radicals, groups and others"*.*
samrotamab védotine	immunoglobuline G1-kappa, anti-[*Homo sapiens* LRRC15 (protéine 15 contenant des répétitions riches en leucine, répétition riche en leucine induite par l'homologue bêta-amyloïde, LIB)], anticorps monoclonal humanisé et chimérique conjugué à l'auristatine E; chaîne lourde gamma1 (1-450) [VH humanisé (*Homo sapiens* IGHV1-2*02 (77.60%) -(IGHD) -IGHJ5*01 (86.7%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), charnière (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfure avec la chaîne légère kappa chimérique (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dimère (229-229'':232-232'')-bisdisulfure ; conjugué sur 2 cystéinyl en moyenne, au monométhylauristatine E (MMAE), via un linker clivable de type maléimidocaproyl-valyl-citrullinyl-p-aminobenzyloxycarbonyl (mc-val-cit-PABC) Pour la partie *védotine*, veuillez-vous référer au document *"INN for pharmaceutical substances: Names for radicals, groups and others"*.*
samrotamab vedotina	inmunoglobulina G1-kappa, anti-[*Homo sapiens* LRRC15 (proteína 15 que contiene las repeticiones ricas en leucina, repetición rica en leucina inducida por el homólogo beta-amiloide, LIB)], anticuerpo monoclonal humanizado y quimérico conjugado con la auristatina E; cadena pesada gamma1 (1-450) [VH humanizado (*Homo sapiens* IGHV1-2*02 (77.60%) -(IGHD) -IGHJ5*01 (86.7%9) [8.8.13] (1-120) -*Homo sapiens* IGHG1*01 (CH1 (121-218), bisagra (219-233), CH2 (234-343), CH3 (344-448), CHS (449-450)) (121-450)], (223-214')-disulfuro con la cadena ligera kappa quimérica (1'-214') [*Mus musculus* V-KAPPA (IGKV10-96*01 (85.30%) -IGKJ1*01 (91.7%)/*Homo sapiens* IGKV1-39*01 (84.2%) -IGKJ4*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')]; dímero (229-229'':232-232'')-bisdisulfuro ; conjugado bajo una media de 2 cisteinil, con la monometilauristatina E (MMAE), a través de un enlace escindible del tipo maleimidocaproil-valil-citrullinil-p-aminobenciloxicarbonil (mc-val-cit-PABC) Para la fracción *vedotina*, se pueden dirigir al documento "*INN for pharmaceutical substances: Names for radicals, groups and others*"*.

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVQSGAE VKKPGASVKV SCKASGYKFS SYWIEWVKQA PGQGLEWIGE  50
ILPGSDTTNY NEKFKDRATF TSDTSINTAY MELSRLRSDD TAVYYCARDR 100
GNYRAWFGYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GGAVKFLIYY  50
TSRLHSGVPS RFSGSGSGTD YTLTISSLQP EDFATYFCQQ GEALPWTFGG 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22''-96'' 147''-203'' 264''-324'' 370''-428''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) * 223-214' 223''-214'''
Inter-H-H (h 11, h 14) * 229-229'' 232-232''
*One or two of the inter-chain disulfide bridges are not present, an average of 2 cysteinyl being conjugated each via a thioether bond to a drug linker.
*Un ou deux des ponts disulfures inter-chaînes ne sont pas présents, 2 cystéinyl en moyenne étant chacun conjugué via une liaison thioéther à un linker-principe actif.
*Faltan uno o dos puentes disulfuro inter-catenarios, una media de 2 cisteinil está conjugada a conectores de principio activo.

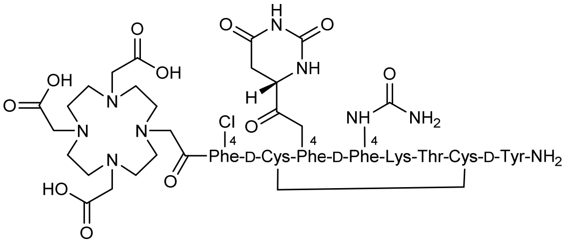
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
G0F, G1F

C-terminal lysine clipping:
H CHS K2: 450, 450''

satoreotidum tetraxetanum

satoreotide tetraxetan	S^2,S^7-cyclo[4-chloro-*N*-{[4,7,10-tris(carboxymethyl)-1,4,7,10-tetraazacyclododecan-1-yl]acetyl}-L-phenylalanyl-D-cysteinyl-4-[(4*S*)-2,6-dioxo-1,3-diazinane-4-carboxamido]-L-phenylalanyl-4-(carbamoylamino)-D-phenylalanyl-L-lysyl-L-threonyl-L-cysteinyl-D-tyrosinamide]
satoréotide tétraxétan	S^2,S^7-cyclo[4-chloro-*N*-{[4,7,10-tris(carboxyméthyl)-1,4,7,10-tétraazacyclododécan-1-yl]acétyl}-L-phénylalanyl-D-cystéinyl-4-[(4*S*)-2,6-dioxo-1,3-diazinane-4-carboxamido]-L-phénylalanyl-4-(carbamoylamino)-D-phénylalanyl-L-lysyl-L-thréonyl-L-cystéinyl-D-tyrosinamide]
satoreotida tetraxetán	S^2,S^7-ciclo[4-cloro-*N*-{[4,7,10-tris(carboximetil)-1,4,7,10-tetraazaciclododecan-1-il]acetil}-L-fenilalanil-D-cisteinil-4-[(4*S*)-2,6-dioxo-1,3-diazinane-4-carboxamido]-L-fenilalanil-4-(carbamoilamino)-D-fenilalanil-L-lisil-L-treonil-L-cisteinil-D-tirosinamida]

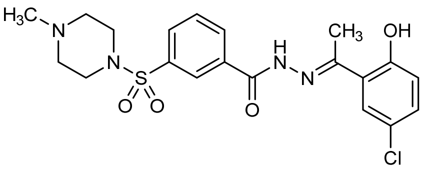
$C_{74}H_{98}ClN_{19}O_{21}S_2$



seclidemstatum

seclidemstat	*N′*-[(1*E*)-1-(5-chloro-2-hydroxyphenyl)ethylidene]-3-(4-methylpiperazine-1-sulfonyl)benzohydrazide
séclidemstat	*N′*-[(1*E*)-1-(5-chloro-2-hydroxyphényl)éthylidene]-3-(4-méthylpipérazine-1-sulfonyl)benzohydrazide
seclidemstat	*N′*-[(1*E*)-1-(5-cloro-2-hidroxifenil)etilideno]-3-(4-metilpiperazina-1-sulfonil)benzohidrazida

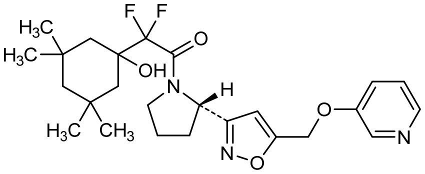
$C_{20}H_{23}ClN_4O_4S$

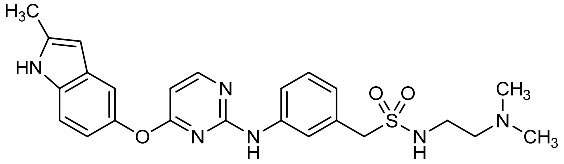


setafrastatum

setafrastat	(5^2*S*)-7,7-difluoro-8^1-hydroxy-8^3,8^3,8^5,8^5-tetramethyl-2-oxa-1(3)-pyridina-4(5,3)-[1,2]oxazola-5(2,1)-pyrrolidina-8(1)-cyclohexanaoctaphan-6-one
sétafrastat	(5^2*S*)-7,7-difluoro-8^1-hydroxy-8^3,8^3,8^5,8^5-tétraméthyl-2-oxa-1(3)-pyridina-4(5,3)-[1,2]oxazola-5(2,1)-pyrrolidina-8(1)-cyclohexanaoctaphan-6-one
setafrastat	(5^2*S*)-7,7-difluoro-8^1-hidroxi-8^3,8^3,8^5,8^5-tetrametil-2-oxa-1(3)-piridina-4(5,3)-[1,2]oxazola-5(2,1)-pirrolidina-8(1)-ciclohexanaoctafan-6-ona

$C_{25}H_{33}F_2N_3O_4$



surufatinibum	
surufatinib	*N*-[2-(dimethylamino)ethyl]-1-[3-({4-[(2-methyl-1*H*-indol-5-yl)oxy]pyrimidin-2-yl}amino)phenyl]methanesulfonamide
surufatinib	*N*-[2-(diméthylamino)éthyl]-1-[3-({4-[(2-méthyl-1*H*-indol-5-yl)oxy]pyrimidin-2-yl}amino)phényl]méthanesulfonamide
surufatinib	*N*-[2-(dimetilamino)etil]-1-[3-({4-[(2-metil-1*H*-indol-5-il)oxi]pirimidin-2-il}amino)fenil]metanosulfonamida
	$C_{24}H_{28}N_6O_3S$
	
sutimlimabum #	
sutimlimab	immunoglobulin G4-kappa, anti-[*Homo sapiens* C1S (complement C1s, complement component 1 subcomponent s)], humanized and chimeric monoclonal antibody; gamma4 heavy chain (1-445) [humanized VH (*Homo sapiens* IGHV3-23*03 (89.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), hinge S10>P (226) (217-228), CH2 L1.2>E (233) (229-338), CH3 (339-443), CHS (444-445)) (118-445)], (132-216')-disulfide with kappa light chain chimeric (1'-216') [V-KAPPA (*Mus musculus* IGKV4-74*01 (82.5%)/*Homo sapiens* IGKV3D-7*01 (78.1%) -*Homo sapiens* IGKJ2*01 (100%)) [7.3.10] (1'-109') -*Homo sapiens* IGKC*01, Km3 A45.1 (155), V101 (193) (110'-216')]; dimer (224-224'':227-227'')-bisdisulfide
sutimlimab	immunoglobuline G4-kappa, anti-[*Homo sapiens* C1S (composant C1s, composant du complément 1 sous-composant s)], anticorps monoclonal humanisé et chimérique; chaîne lourde gamma4 (1-445) [VH humanisé (*Homo sapiens* IGHV3-23*03 (89.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), charnière S10>P (226) (217-228), CH2 L1.2>E (233) (229-338), CH3 (339-443), CHS (444-445)) (118-445)], (132-216')-disulfure avec la chaîne légère kappa chimérique (1'-216') [V-KAPPA (*Mus musculus* IGKV4-74*01 (82.5%)/*Homo sapiens* IGKV3D-7*01 (78.1%) -*Homo sapiens* IGKJ2*01 (100%)) [7.3.10] (1'-109') -*Homo sapiens* IGKC*01, Km3 A45.1 (155), V101 (193) (110'-216')]; dimère (224-224'':227-227'')-bisdisulfure
sutimlimab	inmunoglobulina G4-kappa, anti-[*Homo sapiens* C1S (componente C1s, componente de complemento 1 subcomponente s)], anticuerpo monoclonal humanizado y quimérico;

cadena pesada gamma4 (1-445) [humanizado VH (*Homo sapiens* IGHV3-23*03 (89.8%) -(IGHD) -IGHJ4*01 (100%)) [8.8.11] (1-118) -*Homo sapiens* IGHG4*01 (CH1 (119-216), bisagra S10>P (226) (217-228), CH2 L1.2>E (233) (229-338), CH3 (339-443), CHS (444-445)) (118-445)], (132-216')-disulfuro con la cadena ligera kappa quimérica (1'-216') [V-KAPPA (*Mus musculus* IGKV4-74*01 (82.5%)/*Homo sapiens* IGKV3D-7*01 (78.1%) -*Homo sapiens* IGKJ2*01 (100%)) [7.3.10] (1'-109') -*Homo sapiens* IGKC*01, Km3 A45.1 (155), V101 (193) (110'-216')]; dímero (224-224'':227-227'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVKPGGSLRL SCAASGFTFS NYAMSWVRQA PGKGLEWVAT  50
ISSGGSHTYY LDSVKGRFTI SRDNSKNTLY LQMNSLRAED TALYYCARLF 100
TGYAMDYWGQ GTLVTVSSAS TKGPSVFPLA PCSRSTSEST AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTKTYT 200
CNVDHKPSNT KVDKRVESKY GPPCPPCPAP EFEGGPSVFL FPPKPKDTLM 250
ISRTPEVTCV VVDVSQEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTYRV 300
VSVLTVLHQD WLNGKEYKCK VSNKGLPSSI EKTISKAKGQ PREPQVYTLP 350
PSQEEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG 400
SFFLYSRLTV DKSRWQEGNV FSCSVMHEAL HNHYTQKSLS LSLGK      445
```

Light chain / Chaîne légère / Cadena ligera

```
QIVLTQSPAT LSLSPGERAT MSCTASSSVS SSYLHWYQQK PGKAPKLWIY  50
STSNLASGVP SRFSGSGSGT DYTLTISSLQ PEDFATYYCH QYYRLPPITF 100
GQGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW 150
KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH 200
QGLSSPVTKS FNRGEC                                      216
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

Intra-H (C23-C104) 22-96 145-201 259-319 365-423
22''-96'' 145''-201'' 259''-319'' 365''-423''
Intra-L (C23-C104) 23'-89' 136'-196'
23'''-89''' 136'''-196'''
Inter-H-L (CH1 10-CL 126) 132-216' 132''-216'''
Inter-H-H (h 8, h 11) 224-224'' 227-227''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
295, 295''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

tagraxofuspum #

tagraxofusp

methionyl (1)-*Corynebacterium diphtheriae* toxin fragment (catalytic and transmembrane domains) (2-389, Q388R variant)-His390-Met391-human interleukin 3 (392-524, natural P399S variant) fusion protein, produced in *Escherichia coli*

tagraxofusp

méthionyl (1)-fragment de toxine de *Corynebacterium diphtheriae* (domaines catalytique et transmembranaire) (2-389, variant Q388R)-His390-Met391-interleukine 3 humaine (392-524, variant P399S naturel) protéine de fusion, produite par *Escherichia coli*

tagraxofusp

metionil (1)-fragmento de toxina de *Corynebacterium diphtheriae* (dominios catalíticos y transmembranarios) (2-389, variante Q388R)-His390-Met391-interleukina 3 humana (392-524, variante P399S natural) proteína de fusión, producida por *Escherichia coli*

```
MGADDVVDSS KSFVMENFSS YHGTKPGYVD SIQKGIQKPK SGTQGNYDDD  50
WKGFYSTDNK YDAAGYSVDN ENPLSGKAGG VVKVTYPGLT KVLALKVDNA 100
ETIKKELGLS LTEPLMEQVG TEEFIKRFGD GASRVVLSLP FAEGSSSVEY 150
INNWEQAKAL SVELEINFET RGKRGQDAMY EYMAQACAGN RVRRSVGSSL 200
SCINLDWDVI RDKTKTKIES LKEHGPIKNK MSESPNKTVS EEKAKQYLEE 250
FHQTALEHPE LSELKTVTGT NPVFAGANYA AWAVNVAQVI DSETADNLEK 300
TTAALSILPG IGSVMGIADG AVHHNTEEIV AQSIALSSLM VAQAIPLVGE 350
LVDIGFAAYN FVESIINLFQ VVHNSYNRPA YSPGHKTRPH MAPMTQTTSL 400
KTSWVNCSNM IDEIITHLKQ PPLPLLDFNN LNGEDQDILM ENNLRRPNLE 450
AFNRAVKSLQ NASAIESILK NLLPCLPLAT AAPTRHPIHI KDGDWNEFRR 500
KLTFYLKTLE NAQAQQTTLS LAIF                             524
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
187-202 407-475

tavokinogenum telseplasmidum #

tavokinogene telseplasmid	a DNA plasmid containing genes coding for the human interleukin 12 (IL-12) p35 and p40 subunits that are separated by an internal ribosomal entry site (IRES) and under the control of a single cytomegalovirus (CMV) promoter
tavokinogène telséplasmide	ADN plasmidique contenant les gènes codant pour les sous-unités p35 et p40 de l'interleukine 12 (IL-12) séparés par un site d'entrée interne du ribosome (IRES) et sous le contrôle d'un promoteur de cytomégalovirus (CMV) unique
tavokinogén telseplásmido	un DNA plasmídico que contiene genes que codifican para las subunidades p35 y p40 de la interleukina 12 (IL-12) que están separados por un sitio de entrada ribosómico interno (IRES) y bajo el control de un único promotor de citomegalovirus (CMV)

tavolimabum #

tavolimab	immunoglobulin G1-kappa, anti-[*Homo sapiens* TNFRSF4 (tumor necrosis factor receptor (TNFR) superfamily member 4, OX40, CD134)], humanized and chimeric monoclonal antibody; gamma1 heavy chain (1-451) [chimeric VH (*Mus musculus* IGHV3-8*02 -(IGHD)-*Homo sapiens* IGHJ4*01) [8.7.15] (1-121) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (122-219), hinge (220-234), CH2 (235-344), CH3 (345-449), CHS (450-451)) (122-451)], (224-214')-disulfide with kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-39*01 (88.40%) -IGKJ1*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 (108'-214')]; dimer (230-230":233-233")-bisdisulfide
tavolimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* TNFRSF4 (membre 4 de la superfamille des récepteurs du facteur de nécrose tumorale, OX40, CD134)], anticorps monoclonal humanisé et chimérique; chaîne lourde gamma1 (1-451) [VH chimérique (*Mus musculus* IGHV3-8*02 -(IGHD)-*Homo sapiens* IGHJ4*01) [8.7.15] (1-121) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (122-219), charnière (220-234),CH2 (235-344), CH3 (345-449), CHS (450-451)) (122-451)], (224-214')-disulfure avec la chaîne légère kappa (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (88.40%) -IGKJ1*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 (108'-214')]; dimère (230-230":233-233")-bisdisulfure

tavolimab

inmunoglobulina G1-kappa, anti-[*Homo sapiens* TNFRSF4 (miembro 4 de la superfamilia de los receptores del factor de necrosis tumoral, OX40, CD134)], anticuerpo monoclonal humanizado y quimérico;
cadena pesada gamma1 (1-451) [VH quimérico (*Mus musculus* IGHV3-8*02 -(IGHD)-*Homo sapiens* IGHJ4*01) [8.7.15] (1-121) -*Homo sapiens* IGHG1*03, G1m3 (CH1 (122-219), bisagra (220-234),CH2 (235-344), CH3 (345-449), CHS (450-451)) (122-451)], (224-214')-disulfuro con la cadena ligera kappa (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (88.40%) -IGKJ1*01) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 (108'-214')]; dímero (230-230":233-233")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQESGPG LVKPSQTLSL TCAVYGGSFS SGYWNWIRKH PGKGLEYIGY  50
ISYNGITYHN PSLKSRITIN RDTSKNQYSL QLNSVTPEDT AVYYCARYKY 100
DYDGGHAMDY WGQGTLVTVS SASTKGPSVF PLAPSSKSTS GGTAALGCLV 150
KDYFPEPVTV SWNSGALTSG VHTFPAVLQS SGLYSLSSVV TVPSSSLGTQ 200
TYICNVNHKP SNTKVDKRVE PKSCDKTHTC PPCPAPELLG GPSVFLFPPK 250
PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY 300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP 350
QVYTLPPSRE EMTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP 400
VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG 450
K                                                     451
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDIS NYLNWYQQKP GKAPKLLIYY  50
TSKLHSGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCQQ GSALPWTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                       214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

```
Intra-H (C23-C104)  22-95     148-204     265-325     371-429
                    22"-95"   148"-204"   265"-325"   371"-429"
Intra-L (C23-C104)  23'-88'     134'-194'
                    23'''-88'''   134'''-194'''
Inter-H-L (h 5-CL 126)  224-214'   224"-214'''
Inter-H-H (h 11, h 14)   230-230"   233-233"
```

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
301, 301"
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

tebentafuspum #
tebentafusp

soluble engineered human T cell receptor, dimer of alpha and beta chains, fused at the beta chain, via a linker (254-258), to a humanized immunoglobulin single-chain variable fragment anti-(human CD3), produced in *Escherichia coli*: IG-scFv-TR-BETA (1-500) [humanized V-KAPPA (*Homo sapiens* IGKV3-33*01 (87.2%) -IGKJ1*01 (100%)) [6.3.9] (1-107) -24-mer tetra(tetraglycyl-seryl)-triglycylseryl linker (108-131) -humanized VH (*Homo sapiens* IGHV3-66*01 (76.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.15] (132-253) -5-mer tetraglycyl-seryl linker(254-258) -*Homo sapiens* V-BETA (TRBV19*01 (95.7%) -(TRBD) -TRBJ2-7 (100%)) [5.6.11] (259-370) -*Homo sapiens* C-BETA (TRBC2*01 EX1 1.7-125, EX2 1 (97.7%) S79>C (427), C85.1>A (445), N97>D (459)) (371-500)], disulfide (427-157')with TR-ALPHA chain (1'-195') [*Homo sapiens* V-ALPHA (TRAV17*01 (98.9%) -TRAJ29*01 (100%)) [5.7.9](1'-109') -C-ALPHA (TRAC*01 EX1 1.3-119, N1.2>K (113), T84>C (157) (97.6%)) (110'-195')]

tébentafusp	récepteur des lymphocytes T humain modifié pour être soluble, dimère des chaînes alpha et bêta, fusionné sur la chaîne bêta, via un linker (254-258), au fragment de la chaîne unique variable de l'immunoglobuline humanisée anti-(CD3 humain), produit par *Escherichia coli:* IG-scFv-TR-BETA (1-500) [V-KAPPA humanisé (*Homo sapiens* IGKV3-33*01 (87.2%) -IGKJ1*01 (100%)) [6.3.9] (1-107) -24-mer tétra(tétraglycyl-séryl)-triglycylséryl linker (108-131) -VH humanisé (*Homo sapiens* IGHV3-66*01 (76.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.15] (132-253) -5-mer tétraglycyl-séryl linker (254-258) -*Homo sapiens* V-BETA (TRBV19*01 (95.7%) -(TRBD) -TRBJ2-7 (100%)) [5.6.11] (259-370) -*Homo sapiens* C-BETA (TRBC2*01 EX1 1.7-125, EX2 1 (97.7%) S79>C (427), C85.1>A (445), N97>D (459)) (371-500)], disulfide (427-157') avec la chaîne TR-ALPHA (1'-195') [*Homo sapiens* V-ALPHA (TRAV17*01 (98.9%) -TRAJ29*01 (100%)) [5.7.9](1'-109') -C-ALPHA (TRAC*01 EX1 1.3-119, N1.2>K (113), T84>C (157) (97.6%)) (110'-195')]
tebentafusp	receptor de linfocitos T humanos modificado por ser soluble, heterodímero de las cadenas alfa y beta, fusionados en la cadena beta, a través de un enlace (254-258), con el fragmento de la cadena única variable de la inmunoglobulina humanizada anti-(CD3 humano), producido por *Escherichia coli:* IG-scFv-TR-BETA (1-500) [V-KAPPA humanizado (*Homo sapiens* IGKV3-33*01 (87.2%) -IGKJ1*01 (100%)) [6.3.9] (1-107) -24-mer tetra(tetraglicil-seril)-triglicilseril ligando (108-131) -VH humanizado (*Homo sapiens* IGHV3-66*01 (76.8%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.15] (132-253) -5-mer tetraglicil-seril ligando (254-258) -*Homo sapiens* V-BETA (TRBV19*01 (95.7%) -(TRBD) -TRBJ2-7 (100%)) [5.6.11] (259-370) -*Homo sapiens* C-BETA (TRBC2*01 EX1 1.7-125, EX2 1 (97.7%) S79>C (427), C85.1>A (445), N97>D (459)) (371-500)], disulfuro (427-157') con la cadena TR-ALPHA (1'-195') [*Homo sapiens* V-ALPHA (TRAV17*01 (98.9%) -TRAJ29*01 (100%)) [5.7.9](1'-109') -C-ALPHA (TRAC*01 EX1 1.3-119, N1.2>K (113), T84>C (157) (97.6%)) (110'-195')]

TCR alpha chain / Chaîne alpha TCR / Cadena alfa TCR

```
AQQGEEDPQA LSIQEGENAT MNCSYKTSIN NLQWYRQNSG RGLVHLILIR 50
SNEREKHSGR LRVTLDTSKK SSSLLITASR AADTASYFCA TDGSTPMQFG 100
KGTRLSVIAN IQKPDPAVYQ LRDSKSSDKS VCLFTDFDSQ TNVSQSKDSD 150
VYITDKCVLD MRSMDFKSNS AVAWSNKSDF ACANAFNNSI IPEDT      195
```

Anti-CD3 scFv - TCR beta chain fusion / Anti-CD3 scFv - chaîne bêta TCR /
Anti-CD3 scFv - cadena beta TCR

```
AIQMTQSPSS LSASVGDRVT ITCRASQDIR NYLNWYQQKP GKAPKLLIYY 50
TSRLESGVPS RFSGSGSGTD YTLTISSLQP EDFATYYCQQ GNTLPWTFGQ 100
GTKVEIKGGG GSGGGGSGGG GSGGGGSGGG SEVQLVESGG GLVQPGGSLR 150
LSCAASGYSF TGYTMNWVRQ APGKGLEWVA LINPYKGVST YNQKFKDRFT 200
ISVDKSKNTA YLQMNSLRAE DTAVYYCARS GYYGDSDWYF DVWGQGTLVT 250
VSSGGGGSDG GITQSPKYLF RKEGQNVTLS CEQNLNHDAM YWYRQDPGQG 300
LRLIYYSWAQ GDFQKGDIAE GYSVSREKKE SFPLTVTSAQ KNPTAFYLCA 350
SSWGAPYEQY FGPGTRLTVT EDLKNVFPPE VAVFEPSEAE ISHTQKATLV 400
CLATGFYPDH VELSWWVNGK EVHSGVCTDP QPLKEQPALN DSRYALSSRL 450
RVSATFWQDP RNHFRCQVQF YGLSENDEWT QDRAKPVTQI VSAEAWGRAD 500
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Inter-chain: alpha chain C157 - beta chain C427
Intra-chain:

TCR alpha chain:	23-89	132-182		
scFv-TCR beta chain fusion:	23-88	153-227	281-349	401-466

α1-α195 = engineered T cell receptor (TCR) α chain fragment

β1-β107 = κ light chain fragment V-KAPPA (IGKV1-12 IGKJ1*01)
β108-β131 = artificial 24 aa peptide linker (G4S)4(G3S)
β132-β253 = heavy chain fragment VH (IGHV3-71 IGHJ2*01)
β254-β258 = artificial 5 aa peptide linker G4S
β259-β500 = engineered T cell receptor (TCR) β chain fragment

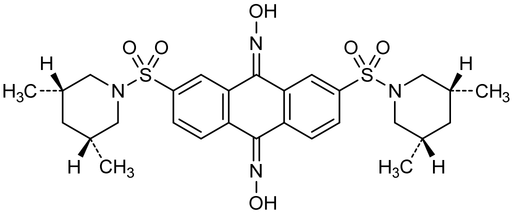
tegavivintum

tegavivint {2,7-bis[(3*R*,5*S*)-3,5-dimethylpiperidine-1-sulfonyl]anthracene-9,10-diylidene}bis(hydroxylamine)

tégavivint {2,7-bis[(3*R*,5*S*)-3,5-diméthylpipéridine-1-sulfonyl]anthracène-9,10-diylidène}bis(hydroxylamine)

tegavivint {2,7-bis[(3*R*,5*S*)-3,5-dimetilpiperidina-1-sulfonil]antraceno-9,10-diilideno}bis(hidroxilamina)

$C_{28}H_{36}N_4O_6S_2$



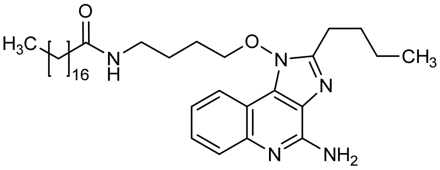
telratolimodum

telratolimod *N*-{4-[(4-amino-2-butyl-1*H*-imidazo[4,5-*c*]quinolin-1-yl)oxy]butyl}octadecanamide

telratolimod *N*-{4-[(4-amino-2-butyl-1*H*-imidazo[4,5-*c*]quinoléin-1-yl)oxy]butyl}octadécanamide

telratolimod *N*-{4-[(4-amino-2-butil-1*H*-imidazo[4,5-*c*]quinolein-1-il)oxi]butil}octadecanamida

$C_{36}H_{59}N_5O_2$



tengonerminum #

tengonermin human tumor necrosis factor (7-163) fused at the N-terminus to a peptide (1-6) ligand of the human CD13 antigen, trimer, produced in *Escherichia coli*;
L-cysteinyl-L-asparaginylglycyl-L-arginyl-L-cysteinylglycyl (1-6, CNGRCG, ligand of the human CD13 antigen)-human tumor necrosis factor soluble form (7-163), non-covalent trimer, produced in *Escherichia coli*

tengonermine facteur de nécrose tumorale humain (7-163), fusionné sur la partie N-terminale, à un peptide (1-6), se liant à l'antigène CD13 humain, trimère, produit dans *Escherichia coli*;
L-cystéinyl-L-asparaginylglycyl-L-arginyl-L-cystéinylglycyl (1-6, CNGRCG, se liant à l'antigène CD13 humain)-forme soluble du facteur de nécrose tumorale humain (7-163), trimère non covalent, produit dans *Escherichia coli*

tengonermina

factor de necrosis tumoral humano (7-163), fusionado en el extremo N-terminal, a un péptido (1-6), unido al antígeno CD13 humano, trímero, producido en *Escherichia coli*;
L-cisteinil-L-asparaginilglicil-L-arginil-L-cisteinilglicil (1-6, CNGRCG, unido al antígeno CD13 humano)-forma soluble del factor de necrosis tumoral humano (7-163), trímero no covalente, producido en *Escherichia coli*

```
CNGRCGVRSS SRTPSDKPVA HVVANPQAEG QLQWLNRRAN ALLANGVELR 50
DNQLVVPSEG LYLIYSQVLF KGQGCPSTHV LLTHTISRIA VSYQTKVNLL 100
SAIKSPCQRE TPEGAEAKPW YEPIYLGGVF QLEKGDRLSA EINRPDYLDF 150
AESGQVYFGI IAL                                        163
```

Disulfide bridges locations / Positions des ponts disulfure / Posiciones de los puentes disulfuro
Intra-chain: 1-5 75-107

tepilamidi fumaras

tepilamide fumarate

2-(diethylamino)-2-oxoethyl and methyl (2*E*)-but-2-enedioate

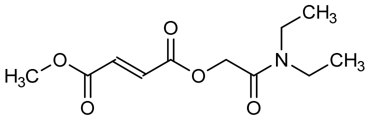
fumarate de tépilamide

(2*E*)-but-2-ènedioate de 2-(diéthylamino)-2-oxoéthyle et de méthyle

fumarato de tepilamida

(2*E*)-but-2-enedioato de 2-(dietilamino)-2-oxoetilo y de metilo

$C_{11}H_{17}NO_5$



tepoditamabum #

tepoditamab

immunoglobulin G1-kappa, anti-[*Homo sapiens* CLEC12A (C-type lectin domain family 12 member A, dendritic cell-associated lectin 2, DCAL-2, myeloid inhibitory C-type lectin-like receptor, MICL, CD371) and anti-[*Homo sapiens* CD3 epsilon (CD3E, Leu-4)], human monoclonal antibody, bispecific;
gamma1 heavy chain anti-CLEC12A (1-447) [*Homo sapiens* VH (IGHV1-46*01 (99.0%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), hinge (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 E12 (357), M14 (359) [L7>D (352), L24>E (369)] (342-446), CHS K2>del (447)) (119-447)]; (221-214')-disulfide with kappa light chain (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100.00%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'-214')];
gamma1 heavy chain anti-CD3E (1''-447'') [*Homo sapiens* VH (IGHV3-33*01 (89.8%) -(IGHD) -IGHJ5*02 (100%)) [8.8.11] (1''-118'') -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), hinge (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 [L7>K (352), T22>K (367)] (342-446), CHS K>del (447)) (119''-447'')], (221''-214''')-disulfide with kappa light chain (1'''-214''') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100%) -IGKJ1*01 (100%)) [6.3.9] (1'''-107''') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'''-214''')]; dimer (227-227'':230-230'')-bisdisulfide

tépoditamab	immunoglobuline G1-kappa, anti-[*Homo sapiens* CLEC12A (membre A de la famille 12 domaine lectine de type C, lectine 2 associée aux cellules dendritiques, DCAL-2, récepteur lectine-like de type C inhibiteur myéloïde, MICL, CD371) et anti-[*Homo sapiens* CD3 epsilon (CD3E, Leu-4)], anticorps monoclonal humain, bispécifique; chaîne lourde gamma1 anti-CLEC12A (1-447) [*Homo sapiens* VH (IGHV1-46*01 (99.0%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), charnière (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 E12 (367), M14 (369) [L7>D (352), L24>E (369)] (342-446), CHS K2>del (447)) (119-447)]; (221-214')-disulfure avec la chaîne légère kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100.00%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; chaîne lourde gamma1 anti-CD3E (1''-447'') [*Homo sapiens* VH (IGHV3-33*01 (89.8%) -(IGHD) -IGHJ5*02 (100%)) [8.8.11] (1''-118'') -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), charnière (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 [L7>K (352), T22>K (367)] (342-446), CHS K>del (447)) (119''-447'')], (221''-214''')-disulfure avec la chaîne légère kappa (1'''-214''') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100%) -IGKJ1*01 (100%)) [6.3.9] (1'''-107''') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'''-214''')]; dimère (227-227'':230-230'')-bisdisulfure
tepoditamab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* CLEC12A (miembro A de la familia 12 dominio lectina de tipo C, lectina 2 asociada con las células dendríticas, DCAL-2, semejante al receptor lectina de tipo C inhibidor mieloide, MICL, CD371) y anti-[*Homo sapiens* CD3 épsilon (CD3E, Leu-4)], anticuerpo monoclonal humano, biespecífico; cadena pesada gamma1 anti-CLEC12A (1-447) [*Homo sapiens* VH (IGHV1-46*01 (99.0%) -(IGHD) -IGHJ4*01 (93.3%)) [8.8.11] (1-118) -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), bisagra (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 E12 (367), M14 (369) [L7>D (352), L24>E (369)] (342-446), CHS K2>del (447)) (119-447)]; (221-214')-disulfuro con la cadena ligera kappa (1'-214') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100.00%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; gamma1 cadena pesada anti-CD3E (1''-447'') [*Homo sapiens* VH (IGHV3-33*01 (89.8%) -(IGHD) -IGHJ5*02 (100%)) [8.8.11] (1''-118'') -*Homo sapiens* IGHG1*03, G1m3 nG1m1 (CH1 R120 (215) (119-216), hinge (217-231), CH2 [L1.2>G (236), G1.1>R (237)] (232-341), CH3 [L7>K (352), T22>K (367)] (342-446), CHS K>del (447)) (119''-447'')], (221''-214''')-disulfuro con la cadena ligera kappa (1'''-214''') [*Homo sapiens* V-KAPPA (IGKV1-39*01 (100%) -IGKJ1*01 (100%)) [6.3.9] (1'''-107''') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191)(108'''-214''')]; dímero (227-227'':230-230'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada anti-CLEC12A

```
QVQLVQSGAE VKKPGASVKV SCKASGYTFT SYYMHWVRQA PGQGLEWMGI  50
INPSGGSTSY AQKFQGRVTM TRDTSTSTVY MELSSLRSED TAVYYCAKGT 100
TGDWFDYWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELGRGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TDPPSREEMT KNQVSLTCEV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
```

Heavy chain / Chaîne lourde / Cadena pesada anti-CD3E

```
QVQLVQSGGG VVQPGRSLRL SCVASGFTFS SYGMHWVRQA PGKGLEWVAA  50
IWYNARKQDY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCTRGT 100
GYNWFDPWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY 150
FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI 200
CNVNHKPSNT KVDKRVEPKS CDKTHTCPPC PAPELGRGPS VFLFPPKPKD 250
TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY 350
TKPPSREEMT KNQVSLKCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD 400
SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG    447
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQSIS SYLNWYQQKP GKAPKLLIYA  50
ASSLQSGVPS RFSGSGSGTD FTLTISSLQP EDFATYYCQQ SYSTPPTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                       214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 145-201 262-322 368-426
22''-96'' 145''-201'' 262''-322'' 368''-426''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 221-214' 221''-214'''
Inter-H-H (h 11, h 14) 227-227'' 230-230''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
298, 298''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

timbetasinum #

timbetasin

human thymosin beta-4, N-terminal acetylated :
3,11,25,31,38-pentakis(de-N^{6}-acetyl)-1,22,30,33-tetrakis(de-O^{3}-phosphono)thymosin β4 (human):
N-acetyl-L-seryl-L-α-aspartyl-L-lysyl-L-prolyl-L-α-aspartyl-L-methionyl-L-alanyl-L-α-glutamyl-L-isoleucyl-L-α-glutamyl-L-lysyl-L-phenylalanyl-L-α-aspartyl-L-lysyl-L-seryl-L-lysyl-L-leucyl-L-lysyl-L-lysyl-L-threonyl-L-α-glutamyl-L-threonyl-L-glutaminyl-L-α-glutamyl-L-lysyl-L-asparaginyl-L-prolyl-L-leucyl-L-prolyl-L-seryl-L-lysyl-L-α-glutamyl-L-threonyl-L-isoleucyl-L-α-glutamyl-L-glutaminyl-L-α-glutamyl-L-lysyl-L-glutaminyl-L-alanylglycyl-L-α-glutamyl-L-serine

timbétasine

thymosine beta-4 humaine, acétylée en son extrémité N-terminale :
3,11,25,31,38-pentakis(dé-N^{6}-acétyl)-1,22,30,33-tétrakis(dé-O^{3}-phosphono)thymosine β4 (humaine):
N-acétyl-L-séryl-L-α-aspartyl-L-lysyl-L-prolyl-L-α-aspartyl-L-méthionyl-L-alanyl-L-α-glutamyl-L-isoleucyl-L-α-glutamyl-L-lysyl-L-phénylalanyl-L-α-aspartyl-L-lysyl-L-séryl-L-lysyl-L-leucyl-L-lysyl-L-lysyl-L-thréonyl-L-α-glutamyl-L-thréonyl-L-glutaminyl-L-α-glutamyl-L-lysyl-L-asparaginyl-L-prolyl-L-leucyl-L-prolyl-L-séryl-L-lysyl-L-α-glutamyl-L-thréonyl-L-isoleucyl-L-α-glutamyl-L-glutaminyl-L-α-glutamyl-L-lysyl-L-glutaminyl-L-alanylglycyl-L-α-glutamyl-L-sérine

timbetasina

timosina beta-4 humana, acetilada en su extremidad N-terminal :
3,11,25,31,38-pentakis(de-*N*^{6}-acetil)-1,22,30,33-tetrakis(de-*O*^{3}-fosfono)timosina β4 (humana):
N-acetil-L-seril-L-α-aspartil-L-lisil-L-prolil-L-α-aspartil-L-metionil-L-alanil-L-α-glutamil-L-isoleucil-L-α-glutamil-L-lisil-L-fenilalanil-L-α-aspartil-L-lisil-L-seril-L-lisil-L-leucil-L-lisil-L-lisil-L-treonil-L-α-glutamil-L-treonil-L-glutaminil-L-α-glutamil-L-lisil-L-asparaginil-L-prolil-L-leucil-L-prolil-L-seril-L-lisil-L-α-glutamil-L-treonil-L-isoleucil-L-α-glutamil-L-glutaminil-L-α-glutamil-L-lisil-L-glutaminil-L-alanilglicil-L-α-glutamil-L-serina

$C_{212}H_{350}N_{56}O_{78}S$

Sequence / Séquence / Secuencia
`SDKPDMAEIE KFDKSKLKKT ETQEKNPLPS KETIEQEKQA GES   43`

Modified residue / résidu modifié / resto modificado
Ser-1: *N*-acetyl-L-serine

tomivosertibum
tomivosertib

6'-[(6-aminopyrimidin-4-yl)amino]-8'-methyl-2'*H*-spiro[cyclohexane-1,3'-imidazo[1,5-*a*]pyridine]-1',5'-dione

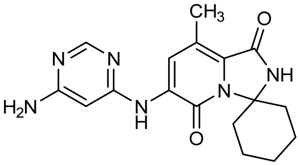
tomivosertib

6'-[(6-aminopyrimidin-4-yl)amino]-8'-méthyl-2'*H*-spiro[cyclohexane-1,3'-imidazo[1,5-*a*]pyridine]-1',5'-dione

tomivosertib

6'-[(6-aminopirimidin-4-il)amino]-8'-metil-2'*H*-spiro[ciclohexano-1,3'-imidazo[1,5-*a*]piridina]-1',5'-diona

$C_{17}H_{20}N_6O_2$



trastuzumabum beta #
trastuzumab beta

immunoglobulin G1-kappa, anti-[*Homo sapiens* ERBB2 (epidermal growth factor receptor 2, receptor tyrosine-protein kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], humanized monoclonal antibody; humanized gamma1 heavy chain (1-449) [humanized VH (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), hinge (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfide with humanized kappa light chain (1'-214') [humanized V-KAPPA (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (229-229":232-232")-bisdisulfide

trastuzumab bêta	immunoglobuline G1-kappa, anti-[*Homo sapiens* ERBB2 (récepteur 2 du facteur de croissance épidermique, récepteur tyrosine-protéine kinase erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticorps monoclonal humanisé; chaîne lourde gamma1 humanisée (1-449) [VH humanisé (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), charnière (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfure avec la chaîne légère kappa humanisée (1'-214') [V-KAPPA humanisé (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dimère (229-229":232-232")-bisdisulfure
trastuzumab beta	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ERBB2 (receptor 2 del factor de crecimiento epidérmico, receptor tirosina-proteína kinasa erbB-2, EGFR2, HER2, HER-2, p185c-erbB2, NEU, CD340)], anticuerpo monoclonal humanizado; cadena pesada gamma1 humanizada (1-449) [VH humanizado (*Homo sapiens* IGHV3-66*01 (81.6%) -(IGHD) -IGHJ4*01 (100%)) [8.8.13] (1-120) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (217) (121-218), bisagra (219-233), CH2 (234-343), CH3 E12 (359), M14 (361) (344-448), CHS K>del (449)) (121-449)], (223-214')-disulfuro con la cadena ligera kappa humanizada (1'-214') [V-KAPPA humanizado (*Homo sapiens* IGKV1-39*01 (86.3%) -IGKJ1*01 (100%)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01 Km3 A45.1 (153), V101 (191) (108'-214')]; dímero (229-229":232-232")-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR  50
IYPTNGYTRY ADSVKGRFTI SADTSKNTAY LQMNSLRAED TAVYYCSRWG 100
GDGFYAMDYW GQGTLVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK 150
DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT 200
YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP 250
KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 350
VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV 400
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPG  449
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASVGDRVT ITCRASQDVN TAVAWYQQKP GKAPKLLIYS  50
ASFLYSGVPS RFSGSRSGTD FTLTISSLQP EDFATYYCQQ HYTTPPTFGQ 100
GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

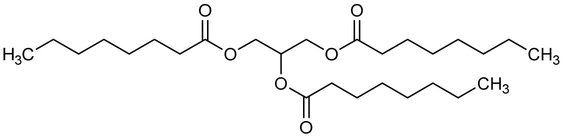
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 147-203 264-324 370-428
22"-96" 147"-203" 264"-324" 370"-428"
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 223-214' 223"-214'''
Inter-H-H (h 11, h 14) 229-229" 232-232"
N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
300, 300"

Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
G0F predominant / prédominant / predominante, A1G0F (0.33 ± 0.05 %), A1G1F (0.35 ± 0.10 %)

tricaprilinum

tricaprilin	propane-1,2,3-triyl trioctanoate
tricapriline	trioctanoate de propane-1,2,3-triyle
tricaprilina	trioctanoato de propano-1,2,3-triilo

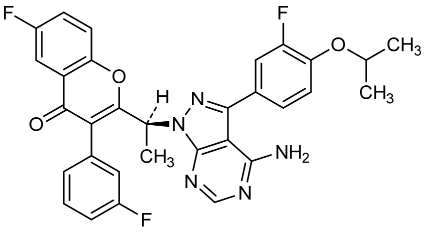
$C_{27}H_{50}O_6$



umbralisibum

umbralisib	2-[(1*S*)-1-{4-amino-3-[3-fluoro-4-(propan-2-yloxy)phenyl]-1*H*-pyrazolo[3,4-*d*]pyrimidin-1-yl}ethyl]-6-fluoro-3-(3-fluorophenyl)-4*H*-1-benzopyran-4-one
umbralisib	2-[(1*S*)-1-{4-amino-3-[3-fluoro-4-(propan-2-yloxy)phényl]-1*H*-pyrazolo[3,4-*d*]pyrimidin-1-yl}éthyl]-6-fluoro-3-(3-fluorophényl)-4*H*-1-benzopyran-4-one
umbralisib	2-[(1*S*)-1-{4-amino-3-[3-fluoro-4-(propan-2-iloxi)fenil]-1*H*-pirazolo[3,4-*d*]pirimidin-1-il}etil]-6-fluoro-3-(3-fluorofenil)-4*H*-1-benzopiran-4-ona

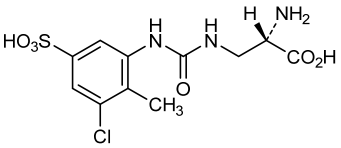
$C_{31}H_{24}F_3N_5O_3$



upacicalcetum

upacicalcet	(2*S*)-2-amino-3-{[(3-chloro-2-methyl-5-sulfophenyl)carbamoyl]amino}propanoic acid
upacicalcet	acide (2*S*)-2-amino-3-{[(3-chloro-2-méthyl-5-sulfophényl)carbamoyl]amino}propanoïque
upacicalcet	ácido (2*S*)-2-amino-3-{[(3-cloro-2-metil-5-sulfofenil)carbamoil]amino}propanoico

$C_{11}H_{14}ClN_3O_6S$



uproleselanum

uproleselan

(2*S*)-2-{2-acetamido-2-deoxy-1-*O*-[(1*R*,2*R*,3*S*,5*R*)-2-[(6-deoxy-α-L-galactopyranosyl)oxy]-3-ethyl-5-(38-oxo-2,5,8,11,14,17,20,23,26,29,32,35-dodecaoxa-39,42-diazatritetracontan-43-oyl)cyclohexyl]-β-D-galactopyranos-3-*O*-yl}-3-cyclohexylpropanoic acid

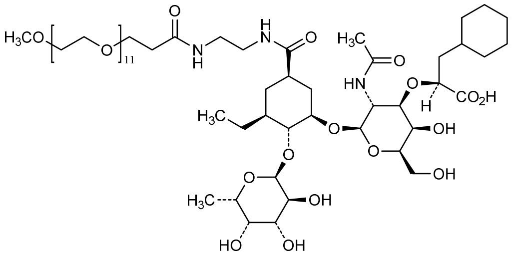
uprolésélan

acide (2*S*)-2-{2-acétamido-2-désoxy-1-*O*-[(1*R*,2*R*,3*S*,5*R*)-2-[(6-désoxy-α-L-galactopyranosyl)oxy]-3-éthyl-5-(38-oxo-2,5,8,11,14,17,20,23,26,29,32,35-dodécaoxa-39,42-diazatritétracontan-43-oyl)cyclohexyl]-β-D-galactopyranos-3-*O*-yl}-3-cyclohexylpropanoïque

uproleselán

ácido (2*S*)-2-{2-acetamido-2-desoxi-1-*O*-[(1*R*,2*R*,3*S*,5*R*)-2-[(6-desoxi-α-L-galactopiranosil)oxi]-3-etil-5-(38-oxo-2,5,8,11,14,17,20,23,26,29,32,35-dodecaoxa-39,42-diazatritetracontan-43-oil)ciclohexil]-β-D-galactopiranos-3-*O*-il}-3-ciclohexilpropanoico

$C_{60}H_{109}N_3O_{27}$



valanafuspum alfa #

valanafusp alfa

anti-(human insulin receptor) immunoglobulin G1 (chimeric human-*Mus musculus*) fused on both heavy chains (1-443, 1''-443'') to seryl-seryl (444-445, 444''-445'')-human α-L-iduronidase (IUDA) ((1-626) natural variant Gln6 (H452>Q)) (447-1072, 447''-1072''), produced in Chinese hamster ovary (CHO) cells, glycoform alfa:
gamma1 heavy chain fused to IDUA (1-1072) [*Mus musculus* VH (IGHV1S56*01 (91.8%) -(IGHD) -IGHJ3*01 (93.3%)) [8.8.6] (1-113) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (210) (114-211), hinge (212-226), CH2 (227-336), CH3 D12 (352), L14 (354) (337-441), CHS K2>S (443) (442-443)) (114-443) -2-mer diseryl linker (444-445) -*Homo sapiens* IDUA, catalytic glutamates E182 (601), E299 (718) (446-1072)], (216-214')-disulfide with kappa light chain (1'-214') [*Mus musculus* V-KAPPA (IGKV9-120*01 (94.7%) -IGKJ1*01 (91.7%), L9>M (104)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3 A45.1 (153), V101 (191) (108'-214')]; dimer (222-222'':225-225'')-bisdisulfide

valanafusp alfa	immunoglobuline G1 (chimérique humaine-*Mus musculus*) anti-(récepteur à l'insuline humain), fusionnée sur les deux chaînes lourdes (1-443, 1''-443'') à séryl-séryl (444-445, 444''-444'')-α-L-iduronidase humaine (IDUA) (Gln6 variant naturel (H452Q)), produite dans des cellules ovariennes de hamsters chinois (CHO), glycoforme alfa: chaîne lourde gamma1 fusionnée à l'IDUA (1-1072) [*Mus musculus* VH (IGHV1S56*01 (91.8%) -(IGHD) -IGHJ3*01 (93.3%)) [8.8.6] (1-113) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (210) (114-211), charnière (212-226), CH2 (227-336), CH3 D12 (352), L14 (354) (337-441), CHS K2>S (443) (442-443)) (114-443) -2-mer diséryl linker (444-445) -*Homo sapiens* IDUA, glutamates catalytiques E182 (601), E299 (718) (446-1072)], (216-214')-disulfure avec la chaîne légère kappa (1'-214') [*Mus musculus* V-KAPPA (IGKV9-120*01 (94.7%) -IGKJ1*01 (91.7%), L9>M (104)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3A45.1 (153), V101 (191) (108'-214')]; dimère (222-222'':225-225'')-bisdisulfure
valanafusp alfa	inmunoglobulina G1 (quimérica humana-*Mus musculus*) anti-(receptor de la insulina humana), fusionada con las diez cadenas pesadas (1-443, 1''-443'') al seril-seril (444-445, 444''-444'')-α-L-iduronidasa humana (IDUA) ((1-626) Gln6 variante natural (H452Q)), producida en las células ováricas de hamsters chinos (CHO), glicoforma alfa: cadena pesada gamma1 fusionada con la IDUA (1-1072) [*Mus musculus* VH (IGHV1S56*01 (91.8%) -(IGHD) -IGHJ3*01 (93.3%)) [8.8.6] (1-113) -*Homo sapiens* IGHG1*01, G1m17,1 (CH1 K120 (210) (114-211), bisagra (212-226), CH2 (227-336), CH3 D12 (352), L14 (354) (337-441), CHS K2>S (443) (442-443)) (114-443) -2-mer ligante diseril (444-445) -*Homo sapiens* IDUA, glutamatos catalíticos E182 (601), E299 (718) (446-1072)], (216-214')-disulfuro con la cadena ligera kappa (1'-214') *[Mus musculus* V-KAPPA (IGKV9-120*01 (94.7%) -IGKJ1*01 (91.7%), L9>M (104)) [6.3.9] (1'-107') -*Homo sapiens* IGKC*01, Km3A45.1 (153), V101 (191) (108'-214')]; dímero (222-222'':225-225'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
QVQLQQSGPE LVKPGALVKI SCKASGYTFT NYDIHWVKQR PGQGLEWIGW 50
IYPGDGSTKY NEKFKGKATL TADKSSSTAY MHLSSLTSEK SAVYFCAREW 100
AYWGQGTLVT VSAASTKGPS VFPLAPSSKS TSGGTAALGC LVKDYFPEPV 150
TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG TQTYICNVNH 200
KPSNTKVDKK VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP PKPKDTLMIS 250
RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE QYNSTYRVVS 300
VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR EPQVYTLPPS 350
RDELTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT PPVLDSDGSF 400
FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS PGSSSEAPHL 450
VQVDAARALW PLRRFWRSTG FCPPLPHSQA DQYVLSWDQQ LNLAYVGAVP 500
HRGIKQVRTH WLLELVTTRG STGRGLSYNF THLDGYLDLL RENQLLPGFE 550
LMGSASGHFT DFEDKQQVFE WKDLVSSLAR RYIGRYGLAH VSKWNFETWN 600
EPDHHDFDNV SMTMQGFLNY YDACSEGLRA ASPALRLGGP GDSFHTPPRS 650
PLSWGLLRHC HDGTNFFTGE AGVRLDYISL HRKGARSSIS ILEQEKVVAQ 700
QIRQLFPKFA DTPIYNDEAD PLVGWSLPQP WRADVTYAAM VVKVIAQHQN 750
LLLANTTSAF PYALLSNDNA FLSYHPHPFA QRTLTARFQV NNTRPPHVQL 800
LRKPVLTAMG LLALLDEEQL WAEVSQAGTV LDSNHTVGVL ASAHRPQGPA 850
DAWRAAVLIY ASDDTRAHPN RSVAVTLRLR GVPPGPGLVY VTRYLDNGLC 900
SPDGEWRRLG RPVFPTAEQF RRMRAAEDPV AAAPRPLPAG GRLTLRPALR 950
LPSLLLVHVC ARPEKPPGQV TRLRALPLTQ GQLVLVWSDE HVGSKCLWTY 1000
EIQFSQDGKA YTPVSRKPST FNLFVFSPDT GAVSGSYRVR ALDYWARPGP 1050
FSDPVPYLEV PVPRGPPSPG NP                               1072
```

Light chain / Chaîne légère / Cadena ligera

```
DIQMTQSPSS LSASLGERVS LTCRASQDIG GNLYWLQQGP DGTIKRLIYA 50
TSSLDSGVPK RFSGSRSGSD YSLTISSLES EDFVDYYCLQ YSSSPWTFGG 100
GTKMEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNNFY PREAKVQWKV 150
DNALQSGNSQ ESVTEQDSKD STYSLSSTLT LSKADYEKHK VYACEVTHQG 200
LSSPVTKSFN RGEC                                        214
```

Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro
Intra-H (C23-C104) 22-96 140-196 257-317 363-421
22''-96'' 140''-196'' 257''-317'' 363''-421''
Intra-H (IDUA) 472-624 660-900 960-996
472''-624'' 660''-900'' 960''-996''
Intra-L (C23-C104) 23'-88' 134'-194'
23'''-88''' 134'''-194'''
Inter-H-L (h 5-CL 126) 216-214' 216''-214'''
Inter-H-H (h 11, h 14) 222-222'' 225-225''

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4: 293, 293''
IDUA: 529, 609, 755, 791, 834, 870, 529'', 609'', 755'', 791'', 834'', 870''

Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados

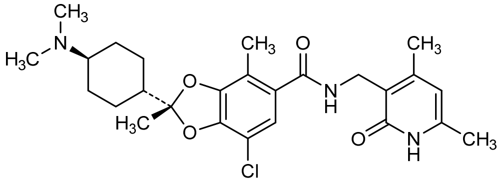
valemetostatum

valemetostat (2*R*)-7-chloro-2-[*trans*-4-(dimethylamino)cyclohexyl]-*N*-[(4,6-dimethyl-2-oxo-1,2-dihydropyridin-3-yl)methyl]-2,4-dimethyl-1,3-benzodioxole-5-carboxamide

valémétostat (2*R*)-7-chloro-2-[*trans*-4-(diméthylamino)cyclohexyl]-*N*-[(4,6-diméthyl-2-oxo-1,2-dihydropyridin-3-yl)méthyl]-2,4-diméthyl-1,3-benzodioxole-5-carboxamide

valemetostat (2*R*)-7-cloro-2-[*trans*-4-(dimetilamino)ciclohexil]-*N*-[(4,6-dimetil-2-oxo-1,2-dihidropiridin-3-il)metil]-2,4-dimetil-1,3-benzodioxol-5-carboxamida

$C_{26}H_{34}ClN_3O_4$



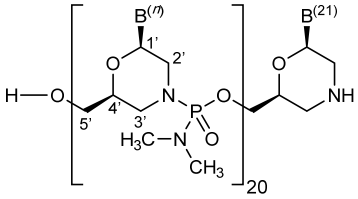
viltolarsenum

viltolarsen *all-P-ambo*-[2',3'-azanediyl-*P*,2',3'-trideoxy-*P*-(dimethylamino)-2',3'-seco](2'-*N*→5')(CCTCCGGTTC TGAAGGTGTT C)

viltolarsen *tout-P-ambo*-[2',3'-azanediyl-*P*,2',3'-tridésoxy-*P*-(diméthylamino)-2',3'-séco](2'-*N*→5')(CCTCCGGTTC TGAAGGTGTT C)

viltolarsén *todo-P-ambo*-[2',3'-azanediil-*P*,2',3'-tridesoxi-*P*-(dimetilamino)-2',3'-seco](2'-*N*→5')(CCTCCGGTTC TGAAGGTGTT C)

$C_{244}H_{381}N_{113}O_{88}P_{20}$



CCTCCGGTTC TGAAGGTGTT C

vopratelimabum #

vopratelimab immunoglobulin G1-kappa, anti-[*Homo sapiens* ICOS (inductible T-cell costimulatory, activation-inducible lymphocyte immunomediatory molecule, AILIM, CD278)], humanized monoclonal antibody;

	gamma1 heavy chain (1-447) [humanized VH (IGHV3-74*01 (88.8%) -(IGHD) -IGHJ5*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (214) (118-215), hinge (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-218')-disulfide with kappa light chain (1'-218') [humanized V-KAPPA (IGKV4-1*01 (84.2%) -IGKJ3*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dimer (226-226'':229-229'')-bisdisulfide
vopratélimab	immunoglobuline G1-kappa, anti-[*Homo sapiens* ICOS (costimulateur inductible du lymphocyte T, molécule immunomédiateur lymphocytaire inductible par activation, AILIM, CD278)], anticorps monoclonal humanisé; chaîne lourde gamma1 (1-447) [VH humanisé (IGHV3-74*01 (88.8%) -(IGHD) -IGHJ5*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (214) (118-215), charnière (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-218')-disulfure avec la chaîne légère kappa (1'-218') [V-KAPPA humanisé (IGKV4-1*01 (84.2%) -IGKJ3*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dimère (226-226'':229-229'')-bisdisulfure
vopratelimab	inmunoglobulina G1-kappa, anti-[*Homo sapiens* ICOS (coestimulador inducible del linfocito T, molécula inmunomediadora linfocitaria inducible por activación, AILIM, CD278)], anticuerpo monoclonal humanizado; cadena pesada gamma1 (1-447) [VH humanizado (IGHV3-74*01 (88.8%) -(IGHD) -IGHJ5*01 (100%)) [8.8.10] (1-117) -*Homo sapiens* IGHG1*03v, G1m3>G1m17, nG1m1 (CH1 R120>K (214) (118-215), bisagra (216-230), CH2 (231-340), CH3 E12 (356), M14 (358) (341-445), CHS (446-447)) (118-447)], (220-218')-disulfuro con la cadena ligera kappa (1'-218') [V-KAPPA humanizado (IGKV4-1*01 (84.2%) -IGKJ3*01 (100%)) [10.3.9] (1'-111') -*Homo sapiens* IGKC*01, Km3 A45.1 (157), V101 (195) (112'-218')]; dímero (226-226'':229-229'')-bisdisulfuro

Heavy chain / Chaîne lourde / Cadena pesada

```
EVQLVESGGG LVQPGGSLRL SCAASGFTFS DYWMDWVRQA PGKGLVWVSN  50
IDEDGSITEY SPFVKGRFTI SRDNAKNTLY LQMNSLRAED TAVYYCTRWG 100
RFGFDSWGQG TLVTVSSAST KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF 150
PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGTQTYIC 200
NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT 250
LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT 350
LPPSREEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS 400
DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK    447
```

Light chain / Chaîne légère / Cadena ligera

```
DIVMTQSPDS LAVSLGERAT INCKSSQSLL SGSFNYLTWY QQKPGQPPKL  50
LIFYASTRHT GVPDRFSGSG SGTDFTLTIS SLQAEDVAVY YCHHHYNAPP 100
TFGPGTKVDI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV 150
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV 200
THQGLSSPVT KSFNRGEC                                   218
```

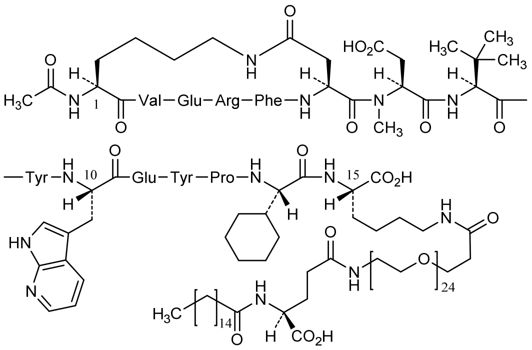
Disulfide bridges location / Position des ponts disulfure / Posiciones de los puentes disulfuro

```
Intra-H (C23-C104)  22-96     144-200     261-321     367-425
                    22''-96''  144''-200''  261''-321''  367''-425''
Intra-L (C23-C104)  23'-92'   138'-198'
                    23'''-92'''  138'''-198'''
Inter-H-L (h 5-CL 126)  220-218'  220''-218'''
Inter-H-H (h 11, h 14)  226-226''  229-229''
```

N-glycosylation sites / Sites de N-glycosylation / Posiciones de N-glicosilación
H CH2 N84.4:
297, 297''
Fucosylated complex bi-antennary CHO-type glycans / glycanes de type CHO bi-antennaires complexes fucosylés / glicanos de tipo CHO biantenarios complejos fucosilados
C-terminal lysine clipping: H CHS K2: 447, 447''

zilucoplanum	
zilucoplan	N^2-acetyl-L-lysyl-L-valyl-L-α-glutamyl-L-arginyl-L-phenylalanyl-L-α-aspartyl-*N*-methyl-L-α-aspartyl-3-methyl-L-valyl-L-tyrosyl-3-(1*H*-pyrrolo[2,3-*b*]pyridin-3-yl)-L-alanyl-L-α-glutamyl-L-tyrosyl-L-prolyl-(2*S*)-2-cyclohexylglycyl-N^6-(3-{ω-[(*N*-hexadecanoyl-L-γ-glutamyl)amino]tetracosakis(oxyethylene)-α-yl}propanoyl)-L-lysine (6→1^6)-lactam
zilucoplan	N^2-acétyl-L-lysyl-L-valyl-L-α-glutamyl-L-arginyl-L-phénylalanyl-L-α-aspartyl-*N*-méthyl-L-α-aspartyl-3-méthyl-L-valyl-L-tyrosyl-3-(1*H*-pyrrolo[2,3-*b*]pyridin-3-yl)-L-alanyl-L-α-glutamyl-L-tyrosyl-L-prolyl-(2*S*)-2-cyclohexylglycyl-N^6-(3-{ω-[(*N*-hexadécanoyl-L-γ-glutamyl)amino]tétracosakis(oxyéthylène)-α-yl}propanoyl)-L-lysine (6→1^6)-lactam
zilucoplán	N^2-acetil-L-lisil-L-valil-L-α-glutamil-L-arginil-L-fenilalanil-L-α-aspartil-*N*-metil-L-α-aspartil-3-metil-L-valil-L-tirosil-3-(1*H*-pirrolo[2,3-*b*]piridin-3-il)-L-alanil-L-α-glutamil-L-tirosil-L-prolil-(2*S*)-2-ciclohexilglicil-N^6-(3-{ω-[(*N*-hexadecanoil-L-γ-glutamil)amino]tetracosakis(oxietileno)-α-il}propanoil)-L-lisina (6→1^6)-lactam

$C_{172}H_{278}N_{24}O_{55}$



AMENDMENTS TO PREVIOUS LISTS
MODIFICATIONS APPORTÉES AUX LISTES ANTÉRIEURES
MODIFICACIONES A LAS LISTAS ANTERIORES

Recommended International Nonproprietary Names (Rec. INN): List 66
Dénominations communes internationales proposées (DCI Rec.): Liste 66
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 66
(WHO Drug Information, Vol. 25, No. 3, 2011)

p. 327 **pracinostatum**
pracinostat *replace the chemical name by the following one*
pracinostat *sustitúyase el nombre químico por el siguiente*

(2*E*)-3-{2-butyl-1-[2-(diethylamino)ethyl]-1*H*-benzimidazol-5-yl}-*N*-hydroxyprop-2-enamide

(2*E*)-3-{2-butil-1-[2-(dietilamino)etil]-1*H*-benzimidazol-5-il}-*N*-hidroxiprop-2-enamida

Recommended International Nonproprietary Names (Rec. INN): List 70
Dénominations communes internationales proposées (DCI Rec.): Liste 70
Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 70
(WHO Drug Information, Vol. 27, No. 3, 2013)

p. 316 **turoctocogum alfa pegolum #**
turoctocog alfa pegol *replace the description by the following one*
turoctocog alfa pégol *remplacer la description par la suivante*
turoctocog alfa pegol *sustitúyase la descripción por la siguiente*

human coagulation factor VIII-(1-750)-(1638-1648)-peptide compound with human coagulation factor VIIIa light chain, glycosylated and pegylated;

$O^{3.750}$-[α-methylpoly(oxyethylene) 5-(acetamido)-3,5-dideoxy-D-*glycero*-α-D-*galacto*-non-2-ulopyranosylonate-(2→4)-α-D-galactopyranosyl-(1→4)-2-(acetamido)-2-deoxy-α-D-galactopyranosyl]-des-(751-1637)-human coagulation factor VIII-(1-1648)-peptide containing 92 kDa factor VIIIa heavy chain compound with human coagulation factor VIIIa light chain glycosylated (glycoform alfa produced in CHO cells)

facteur VIII de coagulation humain-(1-750)-(1638-1648)-peptide associé à la chaîne légère du facteur VIIIa de coagulation humain glycosylés et pégylés;

$O^{3.750}$-[5-(acétamido)-3,5-didésoxy-D-*glycéro*-α-D-*galacto*-non-2-ulopyranosylonate de α-méthylpoly(oxyéthylène)-(2→4)-α-D-galactopyranosyl-(1→4)-2-(acétamido)-2-déoxy-α-D-galactopyranosyl]-dès-(751-1637)-facteur VIII de coagulation humain-(1-1648)-peptide contenant la chaîne lourde de 92 kDa du factor VIIIa associé à la chaîne légère du facteur VIIIa de coagulation humain glycosylés (glycoforme alfa produit par des cellules CHO) factor VIII de coagulación humano-(1-750)-(1638-1648)-péptido asociado a la cadena ligera del factor VIIIa de coagulación humano glicosilados y pegilados;

$O^{3.750}$-[5-(acetamido)-3,5-didesoxi-D-*glicero*-β-D-*galacto*-non-2-ulopiranosilonato de α-metilpoli(oxietileno)-(2→4)-α-D-galactopiranosil-(1→4)-2-(acetamido)-2-desoxi-α-D-galactopiranosil]-des-(751-1637)-factor VIII de coagulación humano-(1-1648)-péptido que contiene la cadena pesada de 92 kDa del factor VIIIa asociado a la cadena ligera del factor VIIIa de coagulación humano glicosilados (glicoforma alfa producido por células CHO)

Recommended International Nonproprietary Names (Rec. INN): List 76 Dénominations communes internationales proposées (DCI Rec.): Liste 76 Denominaciones Comunes Internacionales Propuestas (DCI Rec.): Lista 76

(WHO Drug Information, Vol. 30, No. 3, 2016)

p. 525	**pibrentasvirum**	
	pibrentasvir	*replace the molecular formula by the following one*
	pibrentasvir	*remplacer la formule moléculaire brute par la suivante*
	pibrentasvir	*sustitúyase la fómula molecular por la siguiente*

$C_{57}H_{65}F_5N_{10}O_8$

Electronic structure available on Mednet: http://mednet.who.int/
Structure électronique disponible sur Mednet: http://mednet.who.int/
Estructura electrónica disponible en Mednet: http://mednet.who.int/
* http://www.who.int/medicines/services/inn/publication/en/

Procedure and Guiding Principles / Procédure et Directives / Procedimientos y principios generales

The text of the *Procedures for the Selection of Recommended International Nonproprietary Names for Pharmaceutical Substances* and *General Principles for Guidance in Devising International Nonproprietary Names for Pharmaceutical Substances* will be reproduced in proposed INN lists only.

Les textes de la *Procédure à suivre en vue du choix de dénominations communes internationales recommandées pour les substances pharmaceutiques* et des *Directives générales pour la formation de dénominations communes internationales applicables aux substances pharmaceutiques* seront publiés seulement dans les listes des DCI proposées.

El texto de los *Procedimientos de selección de denominaciones comunes internacionales recomendadas para las sustancias farmacéuticas* y de los *Principios generales de orientación para formar denominaciones comunes internacionales para sustancias farmacéuticas* aparece solamente en las listas de DCI propuestas.